

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 12, 2003, 22:40:30 ; Search time 9691 Seconds
(without alignments)
11503.326 Million cell updates/sec

Title: US-10-054-678-1
Perfect score: 2725
Sequence: 1 tcagtcgtggccagcctg.....aagtcacacttgggtggc 2725

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 120 summaries

Database : GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_ats.*

12: gb_ey.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_ats.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rnd.*

36: em_htg_man.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2725	100.0	2725	6	AX356102 Sequence
2	2725	100.0	2725	9	HSDBHR
3	2717	99.7	2807	9	BC017174 Homo sapi
4	2425	89.0	2425	9	HSDBHR
5	1940	71.2	1955	9	HSDBHR
6	1805.2	66.2	1812	12	BT007470 Synthetic
7	1702.8	62.5	3842	4	AB029430 Equus cab
8	1498	55.0	2317	4	AF118638 Bos tauru
9	1476.8	54.2	2322	4	BOVADBM
10	1419.2	52.1	1840	4	BOVDBH
11	1412.8	51.8	2195	4	BOVDBH2
12	1236.8	45.4	2274	10	S02000
13	1219.4	44.7	2443	10	RATDOPBHY
14	1016.8	37.3	1092	9	HSDBH12
15	1016.8	37.3	46651	9	AC000404
16	1016.8	37.3	53242	9	AL365494
17	1016.8	37.3	110000	2	AL954350_3
18	1001.2	36.7	110000	2	AL954350_0
19	330	12.1	2037	9	HSDBH1
20	328.4	12.1	37584	9	AC001227
21	326.6	12.0	509	5	CGA251457
22	258.4	9.5	276	9	HSDBH3
23	239.6	8.8	262	9	AF070919
24	228.4	8.4	2894	3	DMTBMR
25	228.4	8.4	73066	10	AL954801
26	228.4	8.4	186208	2	AC010965
27	228.4	8.4	205420	2	AC031762
28	221.6	8.1	663	5	AF075385
29	220	8.1	225079	2	AC126203
30	193	7.1	2037	6	AX347199
31	193	7.1	2037	6	AX348532
32	180	6.6	195	9	HSDBH4
33	179.6	6.6	2037	6	AX347198
34	179.6	6.6	2037	6	AX348531
35	175.8	6.5	2164	10	BC037684
36	174.2	6.4	2903	10	AB041606
37	172	6.3	2796	10	BC025892
38	170	6.2	185	9	HSDBH6
39	166.8	6.1	2906	9	AF129263
40	163.8	6.0	178	9	HSDBH11
41	151.4	5.6	2188	9	BC018756
42	149.2	5.5	162	9	HSDBH7
43	149	5.5	165	9	HSDBH2
44	146.8	5.4	2150	6	AX464056
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46	141.8	5.2	2762	6	BD127343
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55	113	4.1	315362	3	AE003442
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57	105	3.9	2139	9	AF129264
58	101.8	3.7	1860	10	AB065134
59	101	3.7	129616	2	AL935290
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RESULT 2

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 DEFINITION
 ACCESSION X13255
 VERSION X13255.1 GI:30473
 KEYWORDS alternative splicing; dopamine beta-hydroxylase; hydroxylase.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2725)
 AUTHORS Kobayashi, K., Kurosawa, Y., Fujita, K. and Nagatsu, T.
 TITLE Human dopamine beta-hydroxylase gene: two mRNA types having different 3'-terminal regions are produced through alternative polyadenylation

JOURNAL Nucleic Acids Res. 17 (3), 1089-1102 (1989)
 MEDLINE 89160241
 PUBMED 2922261
 REFERENCE 2 (bases 1 to 2725)
 AUTHORS Nagatsuo, T.
 TITLE Direct Submission
 JOURNAL Submitted (14-OCT-1988) Nagatsuo T., Department of Biochemistry,
 Nagoya University, School of Medicine, Nagoya 466, Japan
 COMMENT see also X13256 for type b mRNA
 Map data from Craig et al. Cytogenet. Cell Genet. 48:48-50 (1988).
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 ORIGIN

Query Match 100.0%; Score 2725; DB 9; Length 2725;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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BC017174
LOCUS
DEFINITION
Homo sapiens, dopamine beta-hydroxylase (dopamine
beta-monooxygenase), clone MGC:2350 IMAGE:3163986, mRNA, complete
cda
ACCSSION
BC017174.1 GI:16877892
VERSION
MGC.
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 2807)
Strausberg, R.
Direct Submission
Submitted (05-NOV-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK
COMMENT
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapsb@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G., Brinkley, C., Brooks, S.,
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, Q.L., Masiello, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J.,
Tiongson, E.E., Touchman, J.W., Taurgeon, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 5 Row: 9 Column: 21
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4503260.
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BASE COUNT 589 a 909 c 788 g 521 t
ORIGIN

Query Match 99.7%; Score 2717; DB 9; Length 2807;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2720; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY	121	AGAGCCCCCTCCCTATACATCCCTCTGGAACCGGGGGGTCTCTGGAGCTCTCATGGA	180
DB	135	AGAGCCCCCTCCCTATACATCCCTCTGGAACCGGGGGGTCTCTGGAGCTCTCATGGA	194
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QY	301	GGACCGATGGGACACTGCTATTTTGGGACGCTTGAGAGCGGCTGAGAGGCGATCC	360
DB	315	GGACCGATGGGACACTGCTATTTTGGGACGCTTGAGAGCGGCTGAGAGGCGATCC	374
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DB	555	ACGGCTCGGGCTGACAGTGGGCTGACAGGGTGCAGCTCTCTGAAGGCCAATATCCCCG	614
QY	601	AACCGGATGTCCTCAGCGCTGACCATGAGGTCCAGCTCCCAATATCCAGATCC	660
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DB	735	ACCACATTATCAAGTACGAGCCCATCGTCAACAGGGCAATGAGGCCCTTGTCCACCA	794
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QY	841	ACTCAAGATGAACACCGGACCGCTCAACTACTGCGCCACGCTGCTGGCGCGCTGGCCCC	900
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QY	901	TGGGTGCAAGGCAATTTTACTACCCAGAGGAAGCCGCTTGCCTTCGGGGGTCCAGGGT	960
DB	915	TGGGTGCAAGGCAATTTTACTACCCAGAGGAAGCCGCTTGCCTTCGGGGGTCCAGGGT	974
QY	961	CTTCCAGATATCTCCGCTCGAAGTTTCACTACCAACCAACCACTGGTGTAGTAGAGCGAA	1020
DB	975	CTTCCAGATATCTCCGCTCGAAGTTTCACTACCAACCAACCACTGGTGTAGTAGAGCGAA	1034
QY	1021	ACGACTCTCAGGCATCCGCTTGTACTACACAGCCAAAGCTGCGGCGCTTCAACGCGGGGA	1080
DB	1035	ACGACTCTCAGGCATCCGCTTGTACTACACAGCCAAAGCTGCGGCGCTTCAACGCGGGGA	1094
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QY	1141	TCATCTCTACTGGCTACTGACGGGACCAAGTGCACCCAGCTGGCAATTCACCAACGCGGAGACCGCT	1200
DB	1155	TCATCTCTACTGGCTACTGACGGGACCAAGTGCACCCAGCTGGCAATTCACCAACGCGGAGACCGCT	1214
QY	1201	TCACATCTTCCGCTCTCAGCTCCACACACTGAGTGGGAGAAAGTGGTTCACAGTGC	1260
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DB	1515	AGACGGCTGTCGACGCGCTTCCTGAGAGTATTCACCTCATCAACAGGTTCAACA	1574
QY	1561	ACGAGGATGTTGCACTGCGCTCAGGCGTCCGCTGCTCAGCAGTTCACCTCTGTTCCCT	1620
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QY	1621	GGAACTCTTCAACCGGAGCTGTAAGGCTGTAAGCTTCGCGCCCATCTCCATGC	1680
DB	1635	GGAACTCTTCAACCGGAGCTGTAAGGCTGTAAGCTTCGCGCCCATCTCCATGC	1694
QY	1681	ACTCAACAAAGTCTCAGCGCTCCGCTTCAGAGGTCGTAAGGCTTCGAGCCCTTCGCCA	1740
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QY	1861	CCCGCTCTCTCAGTGTCTTCCCTGTGGGCTCACACCGGCACTGTGCACTTACTCTGCGAC	1920
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Qy	2341	GGAGGACAGGACAGGCAATTTAGCTAGTTAGAGACTCCGCTGGGAAATTTGCTCCATTCTG	2400
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Qy	2521	AGACACAGCTTGTCTTCTGCGGTGGGGCCAGCGCTGAAACAGACCGGGTGGAGTCAGG	2580
Db	2535	AGACACAGCTTGTCTTCTGCGGTGGGGCCAGCGCTGAAACAGACCGGGTGGAGTCAGG	2594
Qy	2581	GCTGTGCTTTCGCGGTGGTCTGCACTTAGGAGTGTGCTTGGCGGGCCATTTCACA	2640
Db	2595	GCTGTGCTTTCGCGGTGGTCTGCACTTAGGAGTGTGCTTGGCGGGCCATTTCACA	2654
Qy	2641	TTCTGACCTCATTCTTCTCATCTGTAACACAGGCTGATCGCTGGCGGCTTAATGAGC	2700
Db	2655	TTCTGACCTCATTCTTCTCATCTGTAACACAGGCTGATCGCTGGCGGCTTAATGAGC	2714
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RESULT 4	
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LOCUS	2425 bp mRNA linear PRI 31-MAR-1995
DEFINITION	Human mRNA for dopamine beta-hydroxylase type b (BC 1.14.17.1).
ACCESSION	X13256
VERSION	X13256.1 GI:30477
KEYWORDS	alternative splicing; dopamine beta-hydroxylase; hydroxylase.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	1 (bases 1 to 2425)
JOURNAL	Kobayashi, K., Kurosawa, Y., Fujita, K. and Nagatsu, T.
	Human dopamine beta-hydroxylase gene: two mRNA types having
	different 3'-terminal regions are produced through alternative
	polyadenylation
	Nucleic Acids Res. 17 (3), 1089-1102 (1989)

MEDLINE	89160241	
PUBMED	2922261	
REFERENCE	2 (bases 1 to 2425)	
TITLE	Nagatsu, T.	
AUTHORS	Direct Submission	
JOURNAL	Submitted (14-Oct-1988) Nagatsu T., Department of Biochemistry,	
COMMENT	Nagoya University, School of Medicine, Nagoya 466, Japan	
FEATURES	Map data from Craig et al. Cytogenet. Cell Genet. 48:48-50 (1988).	
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Matches 2425; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
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Db 2341 GGAGCGAGGACAGGCAATTTAGCTAGTGTAGAGCTCGCTGGGAAATTTGCTTCCATTCTG 2400
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Db 2401 AGTAAACAGATATTTTCCGCCACCT 2425

RESULT 5

LOCUS HSDBH 1955 bp mRNA linear PRI 31-MAR-1995
DEFINITION Human mRNA for dopamine beta-hydroxylase (EC 1.14.17.1).
ACCESSION Y00096
VERSION Y00096.1 GI:30455
KEYWORDS dopamine beta-hydroxylase.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE	1 (bases 1 to 1955)
AUTHORS	Lamouroux,A., Vigny,A., Faucon Biguet,N., Darmon,M.C., Franck,R., Henry,J.P. and Mallet,J.
TITLE	The primary structure of human dopamine-ss-hydroxylase: insights into the relationship between the soluble and the membrane-bound forms of the enzyme
JOURNAL	EMBO J. 6, 3921-3937 (1987)
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Matches 1943; Conservative	0; Mismatches 5; Indels 0; Gaps 0;
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Qy	421 CCTGCTTTTCAAGAGGCCCTTTGGCACTCTGCGAATCCCAAGGATTAATCTTCAAGACG 480
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Db 1928 GATCCCCAAGGAACGCCCTGACGCC 1955

BT007470 1812 bp mRNA linear SYN 13-MAY-2003
LOCUS BT007470
DEFINITION Synthetic construct Homo sapiens dopamine beta-hydroxylase
(dopamine beta-monooxygenase) mRNA, partial cds.
ACCESSION BT007470
VERSION 1
KEYWORDS FLI CDNA.
SOURCE synthetic construct
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1812)
AUTHORS Kalline,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M. and Farmer,A.
TITLE Cloning of human full-length CDSs in BD Creator(TM) System Donor
vector
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1812)
AUTHORS Kalline,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M. and Farmer,A.
TITLE Direct Submission
JOURNAL Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow
Circle, Palo Alto, CA 94303, USA
COMMENT This CDS clone is a part of a collection of human full length
expression clones generated by BD Biosciences Clontech and the
Harvard Institute of Proteomics. Each CDS has been cloned in two
forms: with and without stop-codon (to allow fusion with C-terminal
tag). The CDS has been directionally cloned using BD In-Fusion(TM)
cloning system between the SalI and HindIII sites of the pDNR-DUAL
vector. Additional sequences in the clone: 'ACC' after SalI site
and before 'ATG' to provide Kozak consensus sequence; 'GG' after
last codon and before HindIII site to maintain reading frame.
Clone distribution: http://bioinfo.clontech.com/orfclones.
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Query Match 66.2%; Score 1805.2; DB 12; Length 1812;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1807; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy	1279	AGTGGAGATCGTGAACACAGACAACTACACAGCCCTCACTTCAGGAGATCCGCTGCT	1338
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Qy	1339	TGAGAGGTCGTGTGGTTCATCCGGGAGATGTCTATCACTCTGCAGTCAACA	1398
Db	1326	TGAGAGGTCGTGTGTGTCCAGCGGGAGACGTGTCTATCACTCTGCATACAACA	1385
Qy	1399	CGGAAGACCGGAGCTGGCCACAGTGGGGGCTTCGGGATCTCGAGGAGATGTGTGCA	1458
Db	1386	CGGAAGACAGGAGCTGGCCACCGTGGGGGCTTCGGGATCTCGAGGAGATGTGTGCA	1445
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Db	1446	ACTAGTGCATCTACCCCGAGACGCTGGAGTCTGCAAGACGGTGTGGACGGC	1505
Qy	1519	GCTTCTTCGAGAAGTACTTCCACTCATCAACAGGTTCAACACGAGATGTCTGCACT	1578
Db	1506	GCTTCTTCGACAAGTACTTCCGCTCTGTGAACAGGTTCAACACGAGGATGTCTGCACT	1565
Qy	1579	GCCTCAGGCGTCTGTCTCAGAGTTCACTCTGTCTCCCTGGAACTCTTCAACCGCG	1638
Db	1566	GCCTCAGGCGTCTGTCTCAGAGTTTGGCTTCCGCTCCGCTGGAACTCTTCAACCGCG	1625
Qy	1639	ACGTACTGAAGGCCCTGTACAGCTTCGCGCCCATCTCCATGCACTGCAACAGTCTCAG	1698
Db	1626	AGGTGCTCAAGGCCCTGTACGCTTCGCACCATCTCCATGCACTGCAACAGTCTCAG	1685
Qy	1699	CCGTCCGCTTCAGGTTGAATGGAACCTTCAGCCCTTCGCCAAGGTCTATCTCCACATGG	1758
Db	1686	CCGTCCGCTTGGAGGCGAGTGAATTCGCGAGCCCTTCCTTGAGATCGTGTCCAGTTGG	1745
Qy	1759	AAGAGCCCAACCCACAGTCCCAACCGCAGGCGGAGCCCTGCTGGCCCAACCGTTG	1818
Db	1746	AAGAGCCCAACCCCTACTGCCAGCGACGAGCTCAGAGCCCGCGGCCCAACCGTGC	1805
Qy	1819	TCAGCATTTGGTGGGCAAGGCTCAGGGGGACCTACTCTCTCCCGCTCTCT - CCATGCT	1876
Db	1806	TGAACATCAGTGGGGCAAGGCTGAACGTGGGAGTCTCTCTCTCTCCCTCACCATTGCT	1865
Qy	1877	GTCCCTGTGGGCTCACACGGCACGTGCA - CTCCTACTCTGCAGCATCCCATGGAAC	1934

Db	1866	GTCCCTGGGGCTCACAGCAGCCCTGTGTGCACCCCTACTCTGTGAGAGCCCCCATGGAAT	1925
QY	1935	AGCCCTGCACGCCCCAGGATGAAGGGCGAGACACGCGCCCTGCTGCTGAGACACCGTCAA	1994
Db	1926	AGCCAGCAGCAGC-----GAGGGCTGACCAAGCACACCTGAGACACGAGGTCCGG	1975
QY	1995	TCCAGCCTTCTTCCGCCAGGGTCCCTTGCATGGCTGAGAGGGTGTGGGTGC-----CCTGT	2050
Db	1976	TCCAGCTTTCTTCCGCCAGGACCCCTTGCATGGCTGAGAGGGTCCCTGACACTTTTGC	2035
QY	2051	TGACCTACCTTGAGCCAGAGTGGACACGACCTCGTCCATTAAACCCGGCTGACTCAGTG	2110
Db	2036	TGACCCACCGAGGCCAGGTGGACAGGAC-----CCTTCACACCCCTTTGACACAGCAT	2090
QY	2111	CAGGACAGCCCGCACAGTGGTCCAGGGTCCAGCCCTCCGCCAGCCCTG-----TTCCGCC	2166
Db	2091	AAGAGCAACCCCTTTTGGAAAGTCTAGAGTCCAGAGCCCGAGAGCCCTGCCATCTCGCTG	2150
QY	2167	TCACTGGGTGTGGCTGCTTCTGGGACAGGACCATCTGGGCCGGGGTGTGGAAATCAC	2226
Db	2151	GGGCTGGGGGTGCCGCTCTCTCTGGGACAGAGCCCTGACCGGACCGGCCAGACTCCC	2210
QY	2227	CGGGAACGCCCCCGCCCCCGCCCTGCTGCTCC	2258
Db	2211	GGAGCTGTCCCGGCCCGCGCTCCCGACGCCCC	2242
RESULT 9			
LOCUS	BOVADM	2322 bp	mRNA linear MAM 26-APR-1993
DEFINITION	Bovine adrenal dopamine beta-monooxygenase mRNA, complete cds.		
ACCESSION	J02890		
VERSION	J02890.1	GI:162610	
KEYWORDS	dopamine beta-monooxygenase.		
SOURCE	Bos taurus (cow)		
ORGANISM	Bos taurus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.		
AUTHORS	1 (bases 1 to 2322)		
TITLE	Taljanidiz, J., Stewart, L., Smith, A.J. and Klinman, J.P.		
	Structure of bovine adrenal dopamine beta-monooxygenase, as deduced from cDNA and protein sequencing: evidence that the membrane-bound form of the enzyme is anchored by an uncleaved signal peptide		
JOURNAL	Biochemistry 28 (26), 10054-10061 (1989)		
MEDLINE	90148928		
PUBMED	2620060		
COMMENT	Original source text: Bovine adrenal medulla, cDNA to mRNA. Draft entry and printed sequence for [1] kindly submitted by C.Mulligan, (18-NOV-89).		
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BASE COUNT 418 a 818 c 684 g 402 t
ORIGIN

Query Match 54.2%; Score 1476.8; DB 4; Length 2322;
Best Local Similarity 80.7%; Pred. No. 1.5e-265;
Matches 1818; Conservative 0; Mismatches 407; Indels 27; Gaps 7;

Qy	19	TGCGCGCCCGAGCATGCGGGAGGACGCTTCATGTACAGCACAGCAGTGCCCATCTTCC	78
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Qy	79	TGGTCATCTCTGGTGGCGCGACATGACAGGCTCGGCTCCCGGTGAGAGCCCCCTCCCTATC	138
Db	75	TGGTCATCTCTGGTGGCTGACATGACAGGCTCGGCGCGCGAGAGCCCCCTCCCTTCC	134
Qy	139	ACATCCCGCTGGACCCGAGGGTCCCTGGAGCTCTCATGGAATGTGAGCTACACCCAGG	198
Db	135	ACATCCCGCTGGACCCCGAGGGACCCCTGGAGCTGCTCTGGAACATCAGCTATGCGCAGG	194
Qy	199	AGGCCATCCATTTCCAGCTCTGCTGGTGGAGGCTCAAGGCTGGCGTCTGTTGGGATGT	258
Db	195	AGACCATCTACTTCCAGCTCTGCTGGCGGAGCTCAAGGCTGGTGTCTCTGTTGGGATGT	254
Qy	259	CCGACCGTGGCGAGCTTGAGAACCCAGATCTCGTGGTGTCTCTGGACCGATGGGGACACTG	318
Db	255	CGGACCGAGGGAGCTGGAGAACTGCTACTTGGTGGTGTCTCTGGACTGACAGGAGCGCG	314
Qy	319	CCTATTTTGGCGACGCTTGGAGTGACCAAGAGGGGAGATCCACCTGGATCCCCCAGCAGG	378
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Qy	379	ACTACAGCTGCTCCAGTGCAGAGGACCCAGAGGCGCTGACCCCTGTTTCAAGAGGC	438
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Qy	439	CCTTTGGCAGCTCGGACCCCAAGGATTACCTCTATTGAAGCGGCACCTGTCACCTTGGTCT	498
Db	435	CTTTTGGCAGCTGTGACCCCAAGGATTACCTCTATTGAAGCGGCACCTGTCACCTTGGTGT	494
Qy	499	ACGGGATCTTGGAGAGCGTTCGGTCACTGGAGGCGCATCAACGGCTCGGGCGCTGCAGA	558
Db	495	ATGGATCTTGGAGAGCGCTCGGTCGGTGGAGTCCATCAACACATCCGGCTTGACA	554
Qy	559	TGGGGCTGCAGAGGGTGAGCTCTGAAAGCCCAATATCCCGGAAACCGGAGTTGGCCCTCAG	618
Db	555	CGGGGCTGCAGAGGGTGAGCTGTGAAGCCCAAGCATCCCGAAGCCGGCCCTGCGCGCG	614
Qy	619	ACGGTGCACCATGGAGGTCCAGCTCCCAATATCCAGATCCCCAGCCAGGAGACCACTGT	678
Db	615	ACAGTGCACCATGGAGATCGCGCCCGGACGTCTCATCCCGGCGCAGACCACTGT	674
Qy	679	ACTGGTCTCATTAAGGAGCTTCAAGGGCTCTCTCGGCACCAATTAAGTACG	738
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Qy	739	AGCCCATCTGCACCAAGGGCAATGAGGCGCTTGTGCAACCATGGAAAGTCTTCAGTGG	798
Db	735	AGCCCATCTGTACCGAGGCAACGAGGCGCTGTGTGCAACCATGGAGGCTTTTCAGTGG	794
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Db	855	AGCGGCTCAACTTCTGCGGTCAAGTGTGCGCGCTGGGCGCTGGGCGCGCAAGGCTTTT	914
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Db	975	TGGNAGTTCTACTACCAACACCCACTGTGTATAGAGCCGGCGGCGACTCTCTGGGCATCC	1034
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Qy	1099	TGTACAGCCAGTGTGGCCATTCACACCGGAGACCGCTTTCATCTCTACTGGCTACT	1158
Db	1095	CGTACAGCCCGGTGATGGCCATCCCCCGCAGGAGACGGCTTCGCTCTCACCGGCTACT	1154
Qy	1159	GCACGGAAGTGCACCCAGCTGCGCTCTCCCTCCGGGATCCACATCTTCGCCCTCTC	1218
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Qy	1219	AGTCTCACACACCTGACTGGGAGAAAGTGTGTACAGTGTCTGGGTCCGGGACCGCCGG	1278
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Qy	1279	AGTGGGAGATCGTGAACACGAGCAATCACTACAGCCCTCACTTCCAGAGATCCGATGT	1338
Db	1275	AGACAGAGATCGTGAACACGAGGCAACCACTACAGCCACACTTCCAGGAGATCCGATGT	1334
Qy	1339	TGAAGAAGT	1398
Db	1335	TGAAGAAGT	1394
Qy	1399	CGGAAGACCGGGAGCTGGCCACAGTGGGGGCTTCCGGATCTCTGGAGGAGATGTGTGTCA	1458
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Qy	1579	GCCTTCAGGCGTCTGTCTCAGCAGTTCACTCTGTCTTCCCTGGAACTCTCTCAACCGCG	1638
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Qy	1639	ACGTACTGAAGGCGCTGTACAGCTTTCGGGCGCATCTCTCATGCACTGCAACAGTCTCAG	1698
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Qy	1699	CGCTTCGCTTCCAGGGTGAATGGAACCTGCAGCGCCCTGCCCAAGGTCATCTCCACACTGG	1758
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Qy	1759	AAGAGCCCAACCCACAGTGCCTCCACAGCCAGCGCGCGGAGCCCTGTGGCGCCCAACCGT	1818
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Qy	1819	TGAGCATTTGGTGGGGGAAAGGCTGAGGGGGAACCTTCTCTCTCTCTCTCTCTCTCTCTCT	1877
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Db	1875	GTCTCTGGGGCTCACAGCAGCCCTGTGCAACCCCTTACTCTGTGAAGACCCCACTGAATA	1934
Qy	1936	GCCTTCAGCGCCCGAGGATGAAGGGGCGAGACCAACGCGCCCTGTCTGTGAGACCACTCCAAT	1995
Db	1935	GCCTTCAGCGCCCGAGGATGAAGGGGCGAGACCAACGCGCCCTGTCTGTGAGACCACTCCAAT	1994
Qy	1996	CCAGCTTTTCTTCCCCCAGGGT--CCCCTGATGCTGAGAGGGTGTGGGTGCG--CTGT	2050
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QY 2051 TGACCTACCTGGACCGAGTGGACCGACCTCGTCCATTAAACCGGCTGACTCAGTG 2110
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2045 TGACCCACGAGGCCAGGTGGACAGGAC-----CTTGACACACCTTTTGACACAGCAT 2099
QY 2111 CAGGACAGCCCGACACAGTGGTCCAGGGTCCAGCCCTCCGCGACAGCCCTG---TTCCGCC 2166
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2100 AAGAGCAACCCCTTTTGGAGTCTAGAGTCCAGAGCCCGAGAGCCCTGCCATCTCGCTG 2159
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RESULT 10
BOVDBH
LOCUS
DEFINITION
ACCESSION J05160
VERSION
KEYWORDS dopamine beta-hydroxylase.
SOURCE Bos taurus
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 1840)
Lewis, E.J., Allison, S., Fader, D., Claflin, V. and Baizer, L.
Bovine dopamine beta-hydroxylase cDNA. Complete coding sequence and
expression in mammalian cells with vaccinia virus vector
J. Biol. Chem. 265 (2), 1021-1028 (1990)
90110081
1688549
COMMENT
Original source text: Bovine (adult) adrenal medulla, cDNA to mRNA.
Draft entry and computer-readable sequence for [1] kindly submitted
by E.J. Lewis, 29-NOV-1989.
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Query Match
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QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
801 CCGGAGATGACAGCTCCCGCACTTCAGCGGCGCTTCGAGCTCCAAGATGAACCCGAC 860
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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
901 TACCGAGGAGCGCGCTTGTCTTGGGGTTCAGGGTCTTCCAGATATCTTCCGCGCTG 960
QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
981 GAAGTTCTACTACCAACCCACTGTTGATAGAGGAGCAACGACTCTCAGGATCCCG 1040
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
961 GAAGTTCTACTACCAACCCACTGTTGATAGAGGAGCAACGACTCTCAGGATCCCG 1020
QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1041 TTGTACTACACAGGCTGCGCGCTTCAACCGCGGGATCATGAGCTGCGAGCTGGTG 1100
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1021 CTGTACTACAGGCTGCGCTGCGCGCTTTCGAGCGGGGATCATGAGCTGCGAGCTGGCG 1080
QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1101 TACACCGCAGTGTGCGCATTCACACGAGGAGACCGCTTCATCTCTCATCTGGTACTGC 1160

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Db 1081 TACAGCCCGTGATGGCCATCCCCCGCAGAGAGCGGCTTCGTCTCACCGGCTACTGC 1140
Qy 1161 ACGGACAAGTGCACCCAGCTGGCACTGCCTCCCTCCGGGATCCACATCTTTCGCTCTCAG 1220
Db 1141 ACGGACAAGTGCACCCAGCTGGCCCTGCGCCCTCAGGATTCACATCTTTCGCTCTCAG 1200
Qy 1221 CTCCACACACACCTGACTGGGAGAAAGTGTGTCAAGTGTGCTCGGGAGCGGCGGGAG 1280
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Db 1261 ACAGAGATCGTGAACACAGGACAACCACTACAGCCCACTTCCAGGAGATCCGCATGTTG 1320
Qy 1341 AAGAAGTCGTGTCGGTCCATCCGGGAGATGTGCTCATCACTCTCTCCAGGTACCAACAG 1400
Db 1321 AAGAAGTCGTGTCGTGTCAGCGGGAGAGCGTGTCTCATCACTCTTCCACATACCAACAG 1380
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Qy 1641 GTACTGAAGCCCTGTACAGCTTCGCGCCCATCTCCATGACCTGCAACAGTCTCTCAGCC 1700
Db 1621 GTGCTCAAGCCCTGTACAGCTTCGCACTCTGCACTCTGCACTGCAACAGGCTCTCGCC 1680
Qy 1701 GTCCGCTTCCAGGTTGAATGGAACCTGCAGCCCTGCGCCCAAGGTCTCATCTCAGACTGGAA 1760
Db 1681 GTCCGCTTCCAGGTTGAATGGAATCGGAGCCCTGCGCTGCTGATCGTGTCCAGTTGGAA 1740
Qy 1761 GAGCCACCCACAGTCCGCCACAGCGAGGCGGAGGAGGCTGTGTCGCCGCCACCGTTGTC 1820
Db 1741 GAGCCACCCCTCACTCCCGCAGCGAGGCTCAGAGCCCGCGGCCCGCCACCGTCTG 1800
Qy 1821 AGCATTGCTGGGCGCAAGGCTGAGGGGAGACCTACTCTCT 1860
Db 1801 ACATCAGTGGGCGCAAGGCTGAACGTGGGAGTCTCTCT 1840
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RESULT 11

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BOVDBHZ
LOCUS BOVDHZ 2195 bp mRNA linear MAM 27-APR-1993
DEFINITION Bovine dopamine beta-hydroxylase mRNA, complete cds.
ACCESSION J02909
VERSION J02909.1 GI:162964
KEYWORDS dopamine beta-hydroxylase.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 2195)
Wang, N., Southan, C., DeWolf, W.E. Jr., Wells, T.N., Kruse, L.I. and
Leatherbarrow, R.J.
Bovine dopamine beta-hydroxylase, primary structure determined by
cDNA cloning and amino acid sequencing
JOURNAL Biochemistry 29 (27), 6466-6474 (1990)
MEDLINE 91002542
PUBMED 2207088
COMMENT Original source text: Bovine, cDNA to mRNA.
FEATURES
Location/Qualifiers
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source

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mRNA

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CDS

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KRPFQCDPNYLIEDGTVHLVYFLEEPSLESINTSLHTGLQRLKPSIPKP
ALPADRTWEIRAPDVLIPQOQTYCYVTELPGDFPHHIVMYEIVTVTGNELVHH
MEVFOCAAFETIPIHFGSPCDKSKWFORLNFCHVLAALWALGAKAFYVPEAGLAFG
PGSSRLRLVHYHNLPLVITGRDSSGIRLYXTARLRRPDAGIMELGLATPYMAIIPD
QETAFVITGCTDKTQLALPASGHIIFSQLHTLTKRVTVLARDRETELINRD
NHYSPHQBELRMUKVSVQPGDLITCTYNTEDRLATVGGFGLIEMCVNVHYV
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ALYGFAPISMHCNRRSAVR"
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BASE COUNT 405 a 764 c 646 g 380 t
ORIGIN

Query Match 51.8%; Score 1412.8; DB 4; Length 2195;
Best Local Similarity 80.7%; Pred. No. 1.3e-253;
Matches 1731; Conservative 0; Mismatches 387; Indels 26; Gaps 6;

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Qy 126 CCCTCCCTATCACATCCCTCCGACCCGAGGGGTCCCTGGAGCTCTCATGAAATGC 185
Db 1 CCCTCCCTCCCTCCATCCCTCCGACCCGAGGGGACCTCGGAAATC 60
Qy 186 AGCTACACCCAGGAGGCATCTTCCAGCTCTCTGTCGGAGGCTCAAGGCTGGCGTC 245
Db 61 AGCTATGCGCAGAGAGACCATCTACTTCCAGCTCTCTGTCGGAGCTCAAGGCTGGTC 120
Qy 246 CTGTTGGAGATGTCGACCGTCGCGAGCTTGAGAACAGATCTCTGTCGTCCTGAGCC 305
Db 121 CTGTTGGAGATGTCGACCGTCGCGAGGAGCTGAGAAATGCTGCTTGGTGGTCTGAGCT 180
Qy 306 GATGGGGACACTGCTCTATTTTGGGAGCCCTGAGTGCACAGAGGGGAGATCCACTG 365
Db 181 GACAGGAGCGGCCCTACTTTGGGAGTGCCTGAGTGACAGAGGGGAGGCTCCACTG 240
Qy 366 GATCCCGCAGCAGACTACACAGCTGCTGAGGTGCAGAGGACCCAGAGGCTGACCCCTG 425
Db 241 GACTCCAGCAGAGATTTACAGCTTCTGCGGACAGAGGACTCAGAGAGGCTGTACTG 300
Qy 426 CTTTCAAGAGGCCCTTTGCGACCTCGACCCCAAGGATTTACCTCATTTGAAGAGCGCACT 485
Db 301 CTCTTCAAGAGGCCCTTTTGGACCTGTGACCCCAAGGATTTACCTCATTCGAGGAGCGCAC 360
Qy 486 GTCCACTTGTCTACGGGATCTCTGAGGAGCGGCTTCTGCTGCTGAGGCGCATCAAGCGC 545
Db 361 GTCCACTTGTGTATGGATTTCTTGGAGGAGCGGCTCGGTCGCTGGAGTCCATCAACACA 420
Qy 546 TCGGGCTTCAGATGGGCTGACAGGGTGCAGCTCTCTGAAGCCCAATATCCCGAAGCCG 605
Db 421 TCGGGCTTCACAGCGGGCTGACAGGGTGCAGCTGCTGAAGCCCGAGCATCCCGAAGCCG 480
Qy 606 GAGTTCCTCTCAGACCGCTGCACCATGAGGCTCCAAAGCTCCCAATATCCAGATCCCCCAGC 665
Db 481 GCCCTGCCCGGACACGCGCACCATGAGATCCGCGGCCCGCCGACGCTCTCATCCCCGGC 540
Qy 666 CAGGACACACGCTACTGCTGCTACATTAAGAGCTTCCAAAGGCTTCTCTCGGCAACAC 725
Db 541 CAGCAGACACGCTACTGCTGCTACGTCAGTCAGCGAGCTCCCGAGCGCTTCCCGCGGAC 600
Qy 726 ATTATCAAGTACGAGCGCCATCGTCACCAAGGGCAATGAGGCCCTTGTGCACACATGGAA 785
Db 601 ATCGTATGTACAGGCCCATCTGTCACCGAGGGCAACAGAGCGCTGGTGACACATGGAG 660
Qy 786 GTCTTCCAGTGGCGCCCGCAGAGATGAGCGTCCCCCACTTTCAGCGGGCCCTCGGACTCC 845
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Query Match		45.4%	Score 1236.8;	DB 10;	Length 2274;
Best Local Similarity		79.5%	Pred. No. 9.6e-221;		
Matches 1463;		Conservative	0;	Mismatches 377;	Indels 0; Gaps 0;
QY	5	TCGCTGGGCGAGCTGCGCGCCCGCCAGCATGCGGGAGGAGCGCTTCATGTACAGCACAGC	64		
DB	311	TTGTTGAGCAGGCTCCCAAGCCCCAGTGTCGCTGAGCGCGCTTCCATGTACGGCACTGC	370		
QY	65	AGTGGCCATCTTCTTGCTCATCTCTGTGTGCGCGCACTGCAGGGCTCGGCTCCCGGTGAGAG	124		
DB	371	TGTGGCCATCTTCTTGCTCATCTCTGTGTGCGCGCACTGCAGGGCTCGGAGCCTCCAGAGAG	430		
QY	125	CCGCTCCCTCATCATCTCCCTTGAGACCCGAGGGGTCCCTGGAGTCTTCATGGAATGT	184		
DB	431	CCGCTTCCCTTACACATCCCTTGAGACCCCGAAGGATTTTAGAGTCTTCATGGAACGT	490		
QY	185	CAGCTACCCAGGAGGCCATCATTTTCAGCTCTCTGTGCGGAGGCTCAAGGCTGGCGT	244		
DB	491	CAGCTATGTCAGAGATCATCATCTTCAGCTCCAGGTGCAAGGGCTGAGGGCTGGGGT	550		
QY	245	CTGTGTTGGAGTGTCCGACCGTGGCGAGCTTGAGAACGCGAGATCTCTGTGTGCTCTGGAC	304		
DB	551	CTGTGTTGGAATGTAGATCGAGAGAGAGATGGAGNAGCGAGATCTCATCATGCTCTGGAG	610		
QY	305	CGATGGGACACTGCTCTATTTTGGGAGCGCTTGAGTGACCAAGAGGGGAGATCCACCT	364		
DB	611	TGATGGGGAAGGGCGCTTACTTTTGGGATGCTGCGAGTGACCGGAAAGGGCAGATCCATCT	670		
QY	365	GGATCCCGCAGCAGCTACAGCTGCTGCGAGGTGCGAGAGACCCAGAGGCGCTGACCT	424		
DB	671	GGATTCGCGAGAGATACAGCTGCTCCAGGCACAGAGAGACTCGAGATGGCGCTGCTCCT	730		
QY	425	GCTTTTCAAGAGCGCTTTTGGCACCTGCGACCCCAAGAGTATCTCATTTGAAGACGCGAC	484		
DB	731	GCTCTTCAAGAGCGCTTTTGTACCTGTGACCCCAAGAGTATGTCTATGAGAGTACAC	790		
QY	485	TGTCCACTTGGTCTACGGGATCTGAGAGAGCGCTTCCGGTCTACTGAGGCGCATCAACGG	544		
DB	791	TGTCCATCTAGTGTATGGGATCTTGGAAAGAGCATTTTCACTGCTGGAGGCCATCAACAC	850		
QY	545	CTCGGCGCTCAGATGGGCTGAGAGGTCAGCTCTTGAAGCCCAATATCCCGNACC	604		
DB	851	CTCAGGCTGTCATACAGGGCTGTGCGGGTGCAGCTTCTGAAGTGTGAGGTCCCGCACTCC	910		
QY	605	GGAGTTGCTCCCTCAGACGCGTGACCATGAGAGTCCCAAGTCTCCCAATATCCAGATCCCGAG	664		
DB	911	ATCCATGCTGAGATGTACAAACCATGATATCCGGGCTCTCGACATCTCATCCCGA	970		
QY	665	CCAGGAGACACGTACTGTGTGTACATTAAGAGCTTCCAAAGGGCTTCTCTCGGACCA	724		
DB	971	CAATGAGCAACGCTACTGTGTGTATATCACTGAGCTACCCCGACGCTTCCCGCGACACCA	1030		
QY	725	CATTATCAGTACAGGCCATCTCACCAGGGCAATGAGGCCCTTGTCCACACATGGA	784		
DB	1031	CATCATCATGTATGAGGCCATTTCTACTGAGGCCAATGAGGCCCTGTGTGCACACATGGA	1090		
QY	785	AGTCTTCCAGTGGCGCCCGAGATGACAGCGTCCCGCACTTCAGCGGGCCCTGCGACTC	844		
DB	1091	GGTCTTCCATATGACAGCTGAGTCTGAGGACTTCCCGCGATTCAACGAGCCCTGTGACTC	1150		
QY	845	CAAGATGAACCCGACCGCTCAACTACTGCGCGCACGTCGTCGGCGCCCTGGGCCCTGGG	904		
DB	1151	CAAAATGAAGCCTGACCGACTCAACTACTGCGCGCACGTCGTCGGCAGCATGGGCCCTGGG	1210		
QY	905	TGCCAAGGCATTTTACTACCAAGAGAGCGCGCTTGCCTTCGGGGTTCAGGGTCCCTC	964		
DB	1211	TGCCAAGGCATTTTACTACCAAAAGAGTGTGTGTCTTTCGGGGGCCCGGGTCCCTC	1270		
QY	965	CAGATATCTCCGCTGGAAGTCTCACTACCAACACCCACTGTGTATAGAAGGAGCAACGA	1024		
DB	1271	CCGGTTTCCCGACTGGAAGTTCATTACCAACACCCAGGAAGATACAGGGCCGGCAGGA	1330		
QY	1025	CTCCTCAGGCATCCGCTTGTGTACTACAGCGCAAGCTGCGCGCTTCAACGCGGGGATCAT	1084		

DB	1331	CTCCTCTGGCATCGCGCTACCTTACACAGCTACTCTCCGACGCTATACGCGGCATCAT	1390		
QY	1085	GGAGCTGGGACTGCTGTACACGCGCAGTGATGGCCATTTCACCAACGCGGAGACCGCTTCAT	1144		
DB	1391	GGAGCTCGGACTGCTGTATACACCTTGTATGCGCATCCCGCTCAGGAGACTGCGCTTGT	1450		
QY	1145	CCTCACTGGCTACTGACGCGACAAGTGACCCAGCTGGCACTGCCTCCCTCCGCGATCCA	1204		
DB	1451	GTTGACCGGCTACTGCACAGACAAGTGACCCAGATGGCACTGCAGGACTCCGGAATCCA	1510		
QY	1205	CATCTTGGCTCTCAGCTTCACACACCTGACTGGGAGAAAGTGTGTACAGTGTGGT	1264		
DB	1511	CATCTTGGCTCTCAGCTTCACACACCTGACTGGGAGAAAGTGTGTACAGTGTGGT	1570		
QY	1265	CGGGAGCGCGGAGTGGGAGATCGTAACACAGGACAATCACTACAGCCCTCACTTCCA	1324		
DB	1571	CAGGGATGGCAAGAGAGGAGGTGAACAGGACAACCACTACAGCCCGCCACTTCCG	1630		
QY	1325	GGAGATCCGCTGTTGAAGAAGTCTGTGCGTCCATCCGCGAGATGTGTCTCATCACTC	1384		
DB	1631	GGAGATCAGAACTGCTGAAGAAGTGTGTGACAGTCTACCCGCGGAGCGTACTCATCACTC	1690		
QY	1385	CTGACGTACAAACGGAAGACCGGGAGCTGGCCACAGTGGGGGGCTTCGCGATCTCGGA	1444		
DB	1691	ATGCACATACAAACAGAAAAAAGACGCTGGCCACAGTGGGGGGTTCGGAATCTTGA	1750		
QY	1445	GGAGATGTGTGCAACTAGTGCACCTACTACCCCGAGACGACGCTGGAGCTTGCAGAC	1504		
DB	1751	GGAGATGTGTGCAACTATGTGCACTACTACCCCGAGACAGAGCTGGAACTCTGCAAGAG	1810		
QY	1505	GGCTGTGGAGCGCGGCTTCTGTCAGAAAGTACTTCCACCTCATCAACAGGTTCAACAACGA	1564		
DB	1811	TGCGGTGGAGCGGCTTCTTACAGAAATACTTCCACATGGTAAACAGGTTTACAGCAGTA	1870		
QY	1565	GGATGTGTGCACTGCGCTTCCAGCGTCCGCTGTCTCAGCAGTTCACCTTCTTCCCTGGA	1624		
DB	1871	GGAGGTCTGCACCTGCGCTTCCAGCGCTCAGTCCCGCCAGCAGTTCCTCTCCGCTGGA	1930		
QY	1625	CTCCTTCAACCGCGAGTACTGAAGCGCTGTACAGCTTTCGCGCCCATCTCCATGCACTG	1684		
DB	1931	CTCTTTCATCGGAATATGCTCAAGGCTCTGTATGACTACGCCCCCTATCTCCATGCACTG	1990		
QY	1685	CAACAAGTCTCTCAGCGCTCCGCTTCCAGGCTGAATGGAACCTGCAGCCCCCTGCCAAGGT	1744		
DB	1991	CAACAAGTCTCTGCTGTCCGCTTCCGCGGTGAGTGGAACTTCGAGCCTTTCGCTAAGAT	2050		
QY	1745	CATCTCCAACCTGGAAGAGCCCAACCCAGTGCCTCCCAACAGCCAGGCGCGAAGCCCTGC	1804		
DB	2051	CACCTCCAGCTGGAAGAACCCACCCACGCTGCCCCATCCGACAGACTCAGAGCCCCGC	2110		
QY	1805	TGCCCCCAGCTGTGTGAGCATTTGGTGGGGCAAGGCTGA	1844		
DB	2111	TAACCCCACTGTGCCCATCACAAAGGAGGAGATGCTGA	2150		

RESULT 13					
RATDOPBYH					
LOCUS	Rattus norvegicus dopamine beta-hydroxylase mRNA, complete cds.	2443 bp	mRNA	linear	ROD 12-JUN-1993
DEFINITION	L12407				
ACCESSION	L12407.1	GI:2945339			
VERSION	dopamine beta-hydroxylase.				
KEYWORDS	Rattus norvegicus (Norway rat)				
SOURCE	Rattus norvegicus				
ORGANISM	Rattus norvegicus				
REFERENCE	1. (bases 1 to 2443)				
AUTHORS	McMahon,A., Geertman,R. and Sabban,E.L.				
TITLE	Rat dopamine beta-hydroxylase: molecular cloning and characterization of the cDNA and regulation of the mRNA by reserpine				

JOURNAL	J. Neurosci. Res. 25 (3), 395-404 (1990)
MEDLINE	90219125
PUBMED	2325165
COMMENT	Original source text: Rattus norvegicus (strain Sprague-Dawley) pheochromocytoma tumor cDNA to mRNA.
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	7. .1869
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3'UTR	1870. .2443
polyA_signal	2309. .2314
polyA_signal	2424. .2429
BASE COUNT	610 a 725 c 595 g 513 t
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Query Match	44.7%; Score 1219.4; DB 10; Length 2443;
Best Local Similarity	76.9%; Pred. No. 1.7e-217;
Matches 1513; Conservative	0; Mismatches 451; Indels 3; Gaps 2;
QY	15 AGCTGCGCGGCCCCAGCATGCGGAGGCGACCTTCATGTACAGACAGCAGTGCGGCATC 74
DB	40 AGCTCCCGAGCCCCAGCTGCTGAGGCGGCTTCATGTATGGCACTGCTGTGGCCATC 99
QY	75 TTCTGGTCTATCTGTGTGGCGGCACTGCGAGGCTCGGCTCCCCGTGAGAGCCCCCTCCCC 134
DB	100 TTCTGGTCTATCTGTGTGGCTGCACTGCGAGGCTCGGAGCTTCGGAGAGCCCCCTTCCCT 159
QY	135 TATCATATCCCTTGACCCGAGGGGTCCCTGGAGCTCTCATGGAAATGTTCAGCTACAC 194
DB	160 TACCACATCCCTCGACCCCTGAAGGAGCTTTTAGAGCTCTCGTGGAACTGAGCTATGAC 219
QY	195 CAGGAGGCCATTCATTTCCAGCTCCTGGTGGGAGGCTCAAGGCTCGGCTCGCTGTTGGG 254
DB	220 CAGGAGATCATCCATCTCCAGCTCCAGGTCCAGGTCGAAGGCGGAGGGCTGGGTCTGTCGGA 279
QY	255 ATGTCGACCGTGGCGAGCTTGAGAACGCGAGATCTCGTGGTGTCTGCGACCGATGGGGAC 314
DB	280 ATGTCGATCGAGGTGAGATGGAGAACGCGACCTCGTCATGCTCTGGACTGACGGGGAC 339
QY	315 ACTGCTATTTTCGACCGCTGGAGTGACAGAGGGGAGATCCACCTGGATGCCAG 374
DB	340 AGGACCTACTTTTCGACCGCTGGAGTGACAGAGGGTGTCAACAGCCTTATCCCTGTCTTCAAG 399
QY	375 CAGGACTTACCAGCTGTGTCAGGTGTCAGAGGACCCAGAGAGGCTGACCTGCTTTTCAAG 434
DB	400 CAGGACTTACCAGCTGTGTCAGGACAGAGGGTGTCAACAGCCTTATCCCTGTCTTCAAG 459
QY	435 AGGCCCTTTGGCACTGCGACCCCAAGGATTTACCTCATTTGAAGACGGCACTGTCCACTTG 494
DB	460 AGGCCCTTTGTACCTGCGACCCCAAGGATTTATGTCATTGAGGATGACACTGTCCACTTA 519
QY	495 GTCTAGGACTCTGAGGAGGCGGTTCCGGTCACTGAGGCCATCAAGCGCTGGGCGCTG 554

DB	520 GTGTATGGGATCTCTGGAGGAGGCATTTCCAGTCCCTGGAGGCCATCAACACCTCAGGCCTA 579
QY	555 CAGATGGGGCTGCAGAGGGTGCAGCTCTCTGAAGCCCAATATATCCCGAAACGGAGATTGCC 614
DB	580 CATACGGGACTACAGCAGGTGCAGCTTCTGAAGCCTGAGGTCTCTCACTCCAGCCATGCCT 639
QY	615 TCAGACGCGTGCACCATGAGGTCCAAAGTCCCAATATCCAGATATCCCAAGCCAGGAGACC 674
DB	640 GGGATGTACAACCATGATATCCGGGCTCTTGAGCTCTCATCCCCAGCACTGAGACC 699
QY	675 ACGTACTGGTGTACATTAAGGAGCTTCCAAAGGGCTTCTCTCGGCACCACTATTAACAAG 734
DB	700 ACATCTGGTCTATATCACTGAGCTACCCCTACACTTCCCCCGACACACATCATCATG 759
QY	735 TAGGAGCCCATCGTCAACAGGGAATGAGGCCCTTGTCCACACATGAGAAATGCTTTCCAG 794
DB	760 TATGAGGCCATTTGTCAAGGAGGCAATGAGGCCCTGTTGTCACCAATGAGGATCTTCCAA 819
QY	795 TCGGCCCGCAGATGGACAGCGTCCCCCACTTTCAGCGGGCCCTGGGACTCCCAAGATGAA 854
DB	820 TGTACAAATGAGTGTGAGGCCCTTCCCATGTTTCAACGAGCCCTGCGACTCCCAAGATGAA 879
QY	855 CCGAGCCGCTCAACTTACTTCTGCCGCCACGTCGTGGCGCCCTGGGGCTGCGGAGGCA 914
DB	880 CTTGACAGACTCAACTTACTTGTGCCACGTCGTGGCGGCACTGGGCCCTGGGCCCAAGCA 939
QY	915 TTTTACTACCCAGAGGAGCGGCCCTTGCCTTTCGGGGGTTCAGGGTCTCTCCAGATATCTC 974
DB	940 TTTTACTACCCAGAGGAGCGGCCCTTGCCTTTCGGGGAGCTCAGGATCTCTCCCGGTTTCTC 999
QY	975 CGCCTGGAAAGTTTCACTTACCACAAACCACTGGTGTGATAGAGGAGCAAAACGACTCCTCAGGC 1034
DB	1000 CGACTGGAAAGTTTCACTTACCACAAATCCACGAATATACAGGCCCGGCGGCACTCTCTGCG 1059
QY	1035 ATCCGCTTGATCTACACAGCCCAAGCTGCGGCGCTTTCAACCGCGGGATCATGAGGCTGGGA 1094
DB	1060 ATCCGCTTACACTACACAGCTAGTCTCCGACCAATAGGAGGAGGCACTCATGAGGCTTGA 1119
QY	1095 CTGGGTGACACGCCAGTGTATGGCCATTCACACACGGGAGACCGCTTCACTCTCACTGCG 1154
DB	1120 CTGGGTGACACGCCCTTGTATGGCCATTCGCCCTCCTCAGGAGACCACTTTGTTGACTGCG 1179
QY	1155 TACTGCAACGGAACAAGTGCACCCAGCTGCGCTTCCCTCCGGATCCACATCTTCGCGC 1214
DB	1180 TACTGCAACGAGACAGGTGCACCCAGATGCACTGCCGAAATCTGGAAATCGGATCTTGGC 1239
QY	1215 TCTAGCTTCCACACACCTGACTGGGAGAAAGTGTGTCAGAGTGTGTCGGGACGCGC 1274
DB	1240 TCACAGCTCCACACGCACTGACCGGAGGAAAGTGTATCTGTCGTCGCCAGGAGTGGC 1299
QY	1275 CGGGAGTGGGAGATCGTGAACCCAGGACCAATCACTACAGCCCTCACTTCAGGAGATCCGC 1334
DB	1300 CAACAGAGGAAAGTGGTGAACAGAGACCAACCACTACAGCCCCCACTTTTCAGGAGATCAGA 1359
QY	1335 ATGTTTGAAGAGAGTGGTGGTCCATCCGGAGATGTGCTCATCACTCTTCGACGCTAC 1394
DB	1360 ATGCTGAAGATGTGCTGATGTCCACAGGGGATGTCTCATCACTTCGTCACATAC 1419
QY	1395 AACACGGAAGACCGGAGCTGGCCACAGTGGGGGCTTCGGGATCTGAGAGAGATGTGT 1454
DB	1420 AACACAGAAAAACAGGACCAATGGCCACAGTGGGGGGTTTGGAAATCTTGGAGAGATGTC 1479
QY	1455 GTCAACTACGTGCACTTACTCCCGCAGAGCTGGAGCTGCAAGACGGCTGGAC 1514
DB	1480 GTCAACTACGTGCACTTACTTACCCCAAAACAGAGCTGGAGCTTGCAGAGTGCCTGGAT 1539
QY	1515 GCGGCTTCTCTGCAAGTACTTTCACCTCATCAACAGGTTTCAACAGAGGATGTCTGCG 1574
DB	1540 GATGCTTCTCTGCAAGAAATACTTCCACATAGTAAACCGTTCGGCAATGAGGAGTCTGCG 1599
QY	1575 ACCTGCCCTCAGGCGCTCGTGTCTCAGCAGGTTCACCTGTGTTCCCTGGAACTCTCTTCAAC 1634
DB	1600 ACCTGCCCTCAGGCGCTCTGTCTCCCGCAGCAGTTCGCTCTGTGCGCTCTGCTTCTTCAAT 1659

QY 1635 CGCAGCTACTGAAGGCCCTGTACAGCTTCGCGCCCATCTCCATGCACTGCAACAAGTCC 1694
 DB 1660 CGTGATATGCTCAAGGCTTTGTATAACTATGCCCCATCTCTGTGCACTGTAACAAGACC 1719
 QY 1695 TCAGCGCTCCGCTCCAGGCTGAATGAACTGCAAGCCCTTCAGCCCTGCCCAGAGGTATCTCCACA 1754
 DB 1720 TCTCCGCTCCGCTTCCCGGGTAACTGGAACCTGAGCCCTCTGCCTTAATATCACTTCGCA 1779
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 DB 1780 GTGGAAGAACCGACCCACAGCTGCCCCATCCGACAGACTCGGGACCCCGCGCCCTTC 1839
 QY 1815 GTTGTAGCATGTGTGGGGCAAGGCTGAGGGGGACCTACTCTCCCCCTCTCTCCATG 1874
 DB 1840 GTTGTGATCACTACGAGGAGGACACACTGA--GTAATTGTTCTTCAGGCTCTCTCGTTT 1897
 QY 1875 CTGTCCCTGTGGGCTCACACCGGCACTGTGCACTCTACTCTGCGACGATC-CCCATGGAA 1933
 DB 1898 TGTCCCTACTGGGCTCACTCCAGCTCTGCGACCCACATGAAGACCCCTTCATAGAA 1957
 QY 1934 CAGCCCTGCAGCCGACGATGAAGGGCCACACACGCCCTGTGCTG 1980
 DB 1958 TAGTGCTGTTACCTAGGAGGGGTATCACCTTGGAGACACTG 2004

RESULT 14

LOCUS HSD112 1092 bp DNA linear PRI 04-MAY-1990
 DEFINITION Human DNA for dopamine beta-hydroxylase exon 12 (EC 1.14.17.1).
 ACCESSION X13268
 VERSION X13268.1 GI:30462
 KEYWORDS alternative splicing; dopamine beta-hydroxylase; hydroxylase.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1092)
 AUTHORS Kobayashi, K., Kurosawa, Y., Fujita, K. and Nagatsu, T.
 TITLE Human dopamine beta-hydroxylase gene: two mRNA types having
 different 3'-terminal regions are produced through alternative
 polyadenylation
 JOURNAL Nucleic Acids Res. 17 (3), 1089-1102 (1989)
 MEDLINE 89160241
 PUBMED 2922261
 REFERENCE 2 (bases 1 to 1092)
 AUTHORS Nagatsu, T.
 TITLE Direct Submission
 JOURNAL Submitted (14-OCT-1988) Nagatsu T., Department of Biochemistry,
 Nagoya University, School of Medicine, Nagoya 466, Japan
 COMMENT Map data from Craig et al. Cytogenet. Cell Genet. 48:48-50(1988).
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 /mol_type="genomic DNA"
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 /map="9q34"

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Query Match 37.3%; Score 1016.8; DB 9; Length 1092;

Best Local Similarity 99.8%; Pred. No. 1.3e-179;

Matches 1018; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 QY 1766 CACCCCAAGTGGCCCCACAGCCAGGGCCGAGCCCTGTGGCCCCACCGTTGTAGCAT 1825
 DB 63 CACCCCAAGTGGCCCCACAGCCAGGGCCGAGCCCTGTGGCCCCACCGTTGTAGCAT 122
 QY 1826 TGTGGGGGCAAAAGGCTGAGGGGGAGCTACTCTCTCCCTCCCTCCATGCTGTCCCTGTG 1885
 DB 123 TGTGGGGGCAAAAGGCTGAGGGGGAGCTACTCTCTCCCTCCCTCCATGCTGTCCCTGTG 182
 QY 1886 GGCTCACACCGGCACTGTGCACTCTACTCTGCGACGATCCCCATGGAACAGCCCTGCAAG 1945
 DB 183 GGCTCACACCGGCACTGTGCACTCTACTCTGCGACGATCCCCATGGAACAGCCCTGCAAG 242
 QY 1946 CCAGAGTGAAGGGGGCAGACCCAGCCCTGTGCGAGACACAGGTCCAATCCAGCTTCT 2005
 DB 243 CCAGAGTGAAGGGGGCAGACCCAGCCCTGTGCGAGACACAGGTCCAATCCAGCTTCT 302
 QY 2006 TCCCCCAGGGTCCCTGCATGGCTGAGAGGGTGTGGGTGGCCCTGTGACCTTACCTGGAC 2065
 DB 303 TCCCCCAGGGTCCCTGCATGGCTGAGAGGGTGTGGGTGGCCCTGTGACCTTACCTGGAC 362
 QY 2066 CGAGTGGACCAACGACCTCGTCCCATTTAAACCCGGCTGACTCAGTGCAGGGAGACGCCGCA 2125
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 QY 2126 CAGTGTGTCAGGCTCAGCCCTCGCGAGCCCTGTTCCGCTCACTGGGTGTGCTCTGGC 2185
 DB 423 CAGTGTGTCAGGCTCAGCCCTCGCGAGCCCTGTTCCGCTCACTGGGTGTGCTCTGGC 482
 QY 2186 TTCTGGACAGGACCACTGCTGGGCGGGGTGTGGAATCACCGGGAACGCCGCCGCC 2245
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 DB 543 GCCCGCTGCTCCCGGTGTGACGGGTGCGGGTGGCGCTTAAACATTTCTCTCTGAGT 602
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RESULT 15

AC000404/c

LOCUS

AC000404 46651 bp DNA linear PRI 29-MAY-1997

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DEFINITION Genomic sequence from Human 9q34, complete sequence.
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VERSION AC000404.1 GI:2133857
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
Hawkins,T.L., Reeve,M.P., Christoffersen,A., Birren,B.W.,
TITLE Genomic sequence from Human 9q34
JOURNAL Unpublished
REFERENCE 1 (bases 1 to 46651)
AUTHORS Pasman,K.H. and Lander,E.S.
2 (bases 1 to 46651)
Hawkins,T.L., Reeve,M.P., Christoffersen,A., Birren,B.W.,
TITLE Direct Submission
JOURNAL Submitted (08-Apr-1997) Whitehead Institute/MIT Center for Genome
REFERENCE Research, 320 Charles Street, Cambridge, MA 02141, USA
AUTHORS 3 (bases 1 to 46651)
Hawkins,T.L., Reeve,M.P., Christoffersen,A., Birren,B.W.,
TITLE Direct Submission
JOURNAL Submitted (29-MAY-1997) Whitehead Institute/MIT Center for Genome
REFERENCE Research, 320 Charles Street, Cambridge, MA 02141, USA
AUTHORS On May 29, 1997 this sequence version replaced gi:1929451.
The Staden databases, finishing information, and all
chromatographic files used in the assembly of this clone are
available from our anonymous ftp site.
All repeats were identified using RepeatMasker: Smit, A.F.A. &
Green, P. (1996-1997)
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Best Local Similarity 99.8%; Pred. No. 6.8e-180;

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QY	1886	GGCTCACACCGGACTGTGCACTCTACTCTGCGACGATCCCATGGAACAGCCCTGACG	1945
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QY	1946	CCAGAGTGAAGGGCCAGACCAACGCCCTGCTGAGACGATCCCATGGAACAGCCCTGACG	2005
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QY	2186	TTCTGGGACAGGCAACATGCTGGGCGGGGTGTGGAATCAACGGGAACGCCCGCCCC	2245
Db	33413	TTCTGGGACAGGCAACATGCTGGGCGGGGTGTGGAATCAACGGGAACGCCCGCCCC	33472
QY	2246	GCCCGCTGCTCCCGGTGTCAGCGGGTGGGGTGGCGCTTAAACATTTCCCTGCTGAGT	2305
Db	33473	GCCCGCTGCTCCCGGTGTCAGCGGGTGGGGTGGCGCTTAAACATTTCCCTGCTGAGT	33532
QY	2306	GGCTCGTGTTCACAGTGGGCGGCTTCCCTGCGACGGAGCAGCAGCAGCATTTAGCTA	2365
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QY	2366	GTTAGAGACTCGCTGGGAAATTTGCTCCATCTCTGAGTAAACAGATATTTCCGCCACCT	2425
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QY	2606	ACTTAGGAGTGTGCTTGGGCGGGCCATTTACATTTCTGACCCCTCACTTTCTCATCT	2665
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QY	2666	GTAACACCGGCTGATGCGGCTAATGAGCAATAAAGCTCACACTTTGGGCTGGC	2725
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RESULT 17

AL954350.3/c

WPCOMMENT

Sequence split into 6 fragments LOCUS AL954350 Accession AL954350

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AL954350.2	200001	310000
AL954350.3	300001	410000
AL954350.4	400001	510000
AL954350.5	500001	539816

Continuation (4 of 6) of AL954350 from base 300001 (AL954350 Homo sapiens chromosome 9 d

Query Match	37.3%;	Score	1016.8;	DB 2;	Length	110000;
Best Local Similarity	99.8%;	Pred.	No 5.9e-180;			
Matches 1018;	Conservative	0;	Mismatches	2;	Indels	0;
Gaps	0;					

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Db	21243	CACCCACACAGTGCACACAGCAGCGCCGAAAGCCCTGCTGCCCCCACCAGCTTGTGAGAT	21184
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Db	21183	TGTTGGGGGAAAGGCTGAGGGGGACCTACTCTCTCCCTCTCTCATGCTGCTCCTGTG	21124
QY	1886	GGCTCACACGGGCACTGTGCACTCTACTCTGCGACGATCCCATGGAACAGCCCTGACG	1945
Db	21123	GGCTCACACGGGCACTGTGCACTCTACTCTGCGACGATCCCATGGAACAGCCCTGACG	21064
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Db	20823	TTCTGGGACAGCACCATGCTGGGCGGGGTGTGGAATFACCGGGAACGCCCGCCCC	20764
QY	2246	GCCCGCTGCTCCCGGTGTGAGCGGGTGGCGGTGTGGAATFACCGGGAACGCCCGCCCC	2305
Db	20763	GCCCGCTGCTCCCGGTGTGAGCGGGTGGCGGTGTGGAATFACCGGGAACGCCCGCCCC	20704
QY	2306	GGCTCGTGTTCACAGTGGGCGGTTCCCTGCGACGGAGCAGGACCCAGGCAATTTAGCTA	2365
Db	20703	GGCTCGTGTTCACAGTGGGCGGTTCCCTGCGACGGAGCAGGACCCAGGCAATTTAGCTA	20644
QY	2366	GTTAGAGACTCGCTGGGAAATTTGCTCCATTTCCCTGAGTAAACAGATATTTTCGCCACCT	2425
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Db      21052 CCCAGGATGAGGGCCAGACACGCCCTGCTGAGACCGTCCATCCAGCTTCT 21111
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QY      2066  CGAGTGGACACGAGCTCGTCCATTTAAACCCGGCTGACTCAGTGCAGGGACAGCCGCA 2125
Db      21172 CGAGTGGACACGAGCTCGTCCATTTAAACCCGGCTGACTCAGTGCAGGGACAGCTGCA 21231
QY      2126  CAGTGGTCCAGGTCAGCCCTCCGCCAGCCCTGTTCGCCCTCCTGAGTGGCTTGGC 2185
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QY      2186  TTCTGGGACAGGACCATGCTGGGCGGGGTGTGGAAATCAGCGGAAAGCCCGCCCC 2245
Db      21292 TTCTGGGACAGGACCATGCTGGGCGGGGTGTGGAAATCAGCGGAAAGCCCGCCCC 21351
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QY      2422  ACCTAAGGGAGCCCTGACAACTATACCAAAAGAGAGGCGGCAAGATCCAGCG 2481
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QY      2482  GGGCTTCTGGGCGCGGTTCACGTGGGTGGATTTAGTGGATTTAGTGGATTTAGTGG 2541
Db      21592 GGGCTTCTGGGCGCGGTTCACGTGGGTGGATTTAGTGGATTTAGTGGATTTAGTGG 21651
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Db      21712 TGGCACTTAGGAGTGTGCTTGGGCGGCGCAATTCACATTCCTGACCTTCTTCTC 21771
QY      2662  ATCTGTAACACCGGCTGATGCGGTGGGCTAATGAGCCCAATAGCTCAGCTTTGGG 2721
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RESULT 19
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DEFINITION X13257
ACCESSION X13257
VERSION   1
KEYWORDS  alternative splicing; dopamine beta-hydroxylase; hydroxylase.
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
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          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 2037)
AUTHORS   Kobayashi, K., Kurosawa, Y., Fujita, K. and Nagatsu, T.
TITLE     Human dopamine beta-hydroxylase gene: two mRNA types having
          different 3'-terminal regions are produced through alternative
          polyadenylation
          Nucleic Acids Res. 17 (3), 1089-1102 (1989)

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MEDLINE 89160241
PUBMED  2922261
REFERENCE 2 (bases 1 to 2037)
AUTHORS  Nagatsu, T.
TITLE     Direct Submission
JOURNAL  Submitted (14-OCT-1988) Nagatsu T., Department of Biochemistry,
          Nagoya University, School of Medicine, Nagoya 466, Japan
COMMENT  Map data from Craig et al. Cytogenet. Cell Genet. 48:48-50 (1988).
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Db 1760 CAGCAGTGGCCATCTTCTGTGTATCTCTGTGTGCGGCACTGAGGGCTCGGCTCCCCGTG 1819
QY 121 AGAGCCCCCTCCCTTATCACAATCCCTTGGACCCGAGGGGTCCCTGGAGCTCTCATGGA 180
Db 1820 AGAGCCCCCTCCCTTATCACAATCCCTTGGACCCGAGGGGTCCCTGGAGCTCTCATGGA 1879
QY 181 ATGTGAGTACACCCAGGAGGCCATCCATTTCCAGCTCTCTGTGCGGAGGCTCAAGGCTG 240
Db 1880 ATGTGAGTACACCCAGGAGGCCATCCATTTCCAGCTCTCTGTGCGGAGGCTCAAGGCTG 1939
QY 241 CGCTCCTGTTTGGGATGTCGACCGTGGCGAGCTTGAGAACGAGATCTCGTGTGTCT 300
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QY 301 GGACCGATGGGACACTGCCTTATTTTGGCG 330
Db 2000 GGACCGATGGGACACTGCCTTATTTTGGCG 2029

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RESULT 20
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LOCUS    AC001227
DEFINITION Genomic sequence from Human 9q34, complete sequence.
ACCESSION AC001227
VERSION   AC001227.1
KEYWORDS  GI:2133860

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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 37584)
AUTHORS     Hawkins,T.L., Reeve,M.P., Christoffersen,A., Birren,B.W.,
            Pasman,K.H. and Lander,E.S.
TITLE       Genomic sequence from Human 9q34
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 37584)
AUTHORS     Hawkins,T.L., Reeve,M.P., Christoffersen,A., Birren,B.W.,
            Pasman,K.H., Lander,E.S., McKernan,K., Munro,C., Richardson,P.,
            Barna,N., Brown,K., Cooke,P., Daly,M.J., Forrest,C., Fripp,W.J.,
            Gage,D., Geraigery,K., Hagos,B., Jacotot,L., Lane,M., Mackenzie,J.,
            Marquis,N., McDermott,J., Moloney,N., Morrow,J., Nachman,A.,
            Naylor,J., O'Connor,T., Peterson,K., Rollins,G., Spencer,J.,
            Stilwell,J., Stone,C., Strickland,C., Sydney,K., Wilmer,F. and
            Zody,M.
TITLE       Direct Submission
JOURNAL     Submitted (10-APR-1997) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3 (bases 1 to 37584)
AUTHORS     Hawkins,T.L., Reeve,M.P., Christoffersen,A., Birren,B.W.,
            Pasman,K.H., Lander,E.S., McKernan,K., Munro,C., Richardson,P.,
            Barna,N., Chang,A., Cooke,P., Daly,M.J., Forrest,C., Fripp,W.J.,
            Gage,D., Geraigery,K., Hagos,B., Jacotot,L., Lane,M., Mackenzie,J.,
            Marquis,N., McDermott,J., Moloney,N., Morrow,J., Nachman,A.,
            Naylor,J., O'Connor,T., Peterson,K., Rollins,G., Spencer,J.,
            Stilwell,J., Stone,C., Strickland,C., Sydney,K., Wilmer,F. and
            Zody,M.
TITLE       Direct Submission
JOURNAL     Submitted (29-MAY-1997) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On May 29, 1997 this sequence version replaced gi:1932719.
            The Staden databases, finishing information, and all
            chromatographic files used in the assembly of this clone are
            available from our anonymous ftp site.

All repeats were identified using RepeatMasker: Smit, A.F.A. &
Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html.

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Best Local Similarity 99.7%; Pred. No. 2.2e-51;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCAGTCGCTGGGCCAGCCTGCCCGGCCCGCCAGCAGTCGCGGAGGAGGAGCCTTCATGTACAGCA 60
Db 11527 TCAGTCGCTGGGCCAGCCTGCCCGGCCCGCCAGCAGTCGCGGAGGAGGAGCCTTCATGTACAGCA 11468
QY 61 CAGCAGTGGCCCATCTTCCTGGTGCATCCTGGTGGCCGCACATGTCAGGGCTCGGCTCCCCCGTG 120
Db 11467 CAGCAGTGGCCCATCTTCCTGGTGCATCCTGGTGGCCGCACATGTCAGGGCTCGGCTCCCCCGTG 11408

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 Db 11407 AGAGCCCCCTCCCTATACATCCCTGACCCGAGGGTCCCTGAGCTCTCATGGA 11348
 QY 181 ATGTCAGCTACACCCAGAGGCCATCCATTTCCAGCTCTCGTGGAGGCTCAAGGCTG 240
 Db 11347 ATGTCAGCTACACCCAGAGGCCATCCATTTCCAGCTCTCGTGGAGGCTCAAGGCTG 11288
 QY 241 GCGTCCCTGTTGGGATGTCGACCGTGGAGCTTGAGAGCGAGATCTCGTGGTGTCT 300
 Db 11287 GCGTCCCTGTTGGGATGTCGACCGTGGAGCTTGAGAGCGAGATCTCGTGGTGTCT 11228
 QY 301 GGACCGATGGGACACCTGCTATTTTGGG 330
 Db 11227 GGACCGTGGGACACTGCTATTTTGGG 11198

RESULT 21
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 LOCUS Gallus gallus partial mRNA for dopamine beta-hydroxylase.
 DEFINITION
 ACCESSION AJ251457
 VERSION
 AJ251457.1 GI:6983691
 KEYWORDS dopamine beta-hydroxylase.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus

REFERENCE 1
 Ernberger, U., Reissmann, E., Mason, I. and Rohrer, H.
 AUTHORS The expression of dopamine beta-hydroxylase, tyrosine hydroxylase,
 TITLE and Phox2 transcription factors in sympathetic neurons: evidence
 for common regulation during noradrenergic induction and diverging
 regulation later in development

JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 509)
 AUTHORS Ernberger, U.
 TITLE Direct Submission
 JOURNAL Submitted (06-DEC-1999) Ernberger U., Ruprecht-Karls-University,
 Institut f. Anatomie und Zellbiologie III, Im Neuenheimer Feld 307,
 D-69120 Heidelberg, GERMANY

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BASE COUNT 120 a 160 c 125 g 104 t
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Query Match 12.0%; Score 326.6; DB 5; Length 509;
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 Matches 395; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY 720 CACCACATATCAAGTACGAGCCATCGTCACCAAGGGCAATGAGGCCCTTGTCCACAC 779
 Db 1 CACCACATATCAATGATGATGACGAGTATCACAGCGGCAATGAGCCCTAGTCCACCA 60

QY 780 ATGGAAGTCTTCAGTGGCGCCCGAGATGGACAGCGTCCCGACATTCACGCGGCCCTGC 839
 Db 61 ATGGAATCTTCAGTGGCAACCGAGTCTGTCAACATCCCCCATTTACACGGTCAATGT 120

QY 840 GACTCCAAGATGAACCCGACCCCTCAACTACTGCGGCACAGTGTGCGCGCTGGGCC 899
 Db 121 GACTCCAAGATGAAGCCAGAGCAGCTCAACTACTGCGGCAGTGTGCTTGCAGCATGGCC 180
 QY 900 CTGGGTGCCCAAGCATTTTACTACCCAGAGGAAGCGGCTTGCCTTCGCGGGTCCAGGG 959
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 Db 241 TCTCCAGATATTTGGCGCTTGAGATTCTACTACCAATCAACTGATATTCAGAGGGCGC 300
 QY 1020 AACGACTCTCAGGCATCGCTTGTAACACAGCAAGCTGCGGCGCTTCAACGGGGG 1079
 Db 301 CGTGATTCCTCGGGATCCGCTGTACTACAGACAAACTGCGTTCACCATGTGTGGC 360
 QY 1080 ATCATGGAGCTGGGACTGGTGATACCGCCAGTGTATGCCCATTCACACCGGAGACCGCC 1139
 Db 361 ATCATGGAGCTGGGCTTGGTCTACTCACCGCTGATGCGCCGTCGCCCGGGGAGACTGCC 420
 QY 1140 TTCATCCTCACTGGCTACTGCGGACAAAGTGACCCAGCTGGCACTGCTCCCTCCGGG 1199
 Db 421 TTCATCCTCACTGGGTACTGCGACCAAAATGCACCAAGGCACTGCTGAAGTGGG 480
 QY 1200 ATCCACATCTTCGCTCTCAGCTCCACAC 1228
 Db 481 ATCCGATCTTCGCTCCCGAGCTCCACAC 509

RESULT 22

HSD3H3

LOCUS Human DNA for dopamine beta-hydroxylase exon 3 (EC 1.14.17.1).
 DEFINITION
 ACCESSION X13259
 VERSION X13259.1 GI:30464
 KEYWORDS alternative splicing; dopamine beta-hydroxylase; hydroxylase.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 276)
 AUTHORS Kobayashi, K., Kurosawa, Y., Fujita, K. and Nagatsu, T.
 TITLE Human dopamine beta-hydroxylase gene: two mRNA types having
 different 3'-terminal regions are produced through alternative
 polyadenylation

JOURNAL Nucleic Acids Res. 17 (3), 1089-1102 (1989)
 MEDLINE 89160241
 PUBMED 2922261
 REFERENCE 2 (bases 1 to 276)
 AUTHORS Nagatsu, T.
 TITLE Direct Submission

JOURNAL Submitted (14-OCT-1988) Nagatsu T., Department of Biochemistry,
 Nagoya University, School of Medicine, Nagoya 466, Japan
 COMMENT Map data from Craig et al. Cytogenet. Cell Genet. 48:48-50(1988).
 FEATURES Location/Qualifiers

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Query Match 9.5%; Score 258.4; DB 9; Length 276;
 Best Local Similarity 99.6%; Pred. No. 5.8e-38;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 475 AAGAGCGCACTGTCACCTTGGTCTACGGGATCCTGGAGGAGCCGTTCCGGTCACTGGAGG 534
Db 8 AGGAGCGCACTGTCACCTTGGTCTACGGGATCCTGGAGGAGCCGTTCCGGTCACTGGAGG 67

Qy 535 CCATCAACGGCTCGGGGCTGCAGATGGGCTGCAGAGGGTGCAGCTCCTCAAGCCCCAATA 594
Db 68 CCATCAACGGCTCGGGGCTGCAGATGGGCTGCAGAGGGTGCAGCTCCTCAAGCCCCAATA 127

Qy 595 TCCCCGAACCGGAGTTGCTCCCTCAGACGCGTGCCACCATGGAGGTCACAGCTCCCAATATCC 654
Db 128 TCCCCGAACCGGAGTTGCTCCCTCAGACGCGTGCCACCATGGAGGTCACAGCTCCCAATATCC 187

Qy 655 AGATCCCCAGCCAGGACACCGTACTGCTGCTACATTAAGGAGCTTCCAAAGGGCTTCT 714
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Qy 715 CTGGGACCACTATCAAG 734
Db 248 CTGGGACCACTATCAAG 267

RESULT 23
LOCUS AF070919
DEFINITION Macaca mulatta dopamine beta-hydroxylase precursor, mRNA, partial cds.
ACCESSION AF070919
VERSION AF070919.1 GI:3220262
KEYWORDS
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.
1 (bases 1 to 262)
Mayerhofer, A., Smith, G.D., Danilchik, M., Levine, J.E., Wolf, D.P., Dissen, G.A. and Ojeda, S.R.
Oocytes are a source of catecholamines in the primate ovary: evidence for a cell-cell regulatory loop
Proc. Natl. Acad. Sci. U.S.A. 95 (18), 10990-10995 (1998)
93193758
PUBMED 9724817
REFERENCE 2 (bases 1 to 262)
Mayerhofer, A., Smith, G.D., Danilchik, M., Levine, J.E., Wolf, D.P., Dissen, G.A. and Ojeda, S.R.
Direct Submission
Submitted (05-JUN-1998) Neurosciences, Oregon Regional Primate Research Center/Oregon Health Sciences University, 505 NW 185th Ave, Beaverton, OR 97006-3448, USA
Location/Qualifiers
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Query Match 8.8%; Score 239.6; DB 9; Length 262;
Best Local Similarity 94.7%; Pred. No. 1.9e-34;
Matches 248; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 839 CGACTCAAGATGAACCCAGCGCTCACTACTCGCGCAGCTGCTGCGCCCTGGCC 898
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Qy 899 CTGGGTGCCAAGCACTTTTACTACCCAGAGGAGCCGCGCTTCCCTTCGGGGGTCCAGG 958
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Qy 959 GTCTCTCCAGATATCTCGGCTCGAAGTTTCACTACCAACCCACTGCTGATAGAAGACG 1018
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Qy 1019 AAACGACTCTCTAGGATCGCTTGTACTACACGACCAAGCTGGGGGCTTCAACGCGGG 1078
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Qy 1079 GATCATGGAGCTGGGACTGGTG 1100
Db 241 GATCATGGAGCTGGGACTGGTG 262

RESULT 24
LOCUS DMTBHR
DEFINITION D.melanogaster mRNA for tyramine-beta-hydroxylase.
ACCESSION 270316
VERSION 270316.1 GI:1296518
KEYWORDS tyramine-beta-hydroxylase.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 2894)
Monastiriotti, M., Linn, C.E. Jr. and White, K.
Characterization of Drosophila tyramine beta-hydroxylase gene and isolation of mutant flies lacking octopamine
J. Neurosci. 16 (12), 3900-3911 (1996)
36242086
PUBMED 8656284
REFERENCE 2 (bases 1 to 2894)
Monastiriotti, M.
Direct Submission
Submitted (29-MAR-1996) Maria Monastiriotti, Insect Molecular Genetics Group, IMBB, Foundation for Research and Technology, Hellas, Vasilika Vouton, Heraklion, Crete, 71110, Greece
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 Qy 65 AGTGGCCATCTTCTGGTCATCTGTGGTGGCGGCGACATGCGAGGCTCGGCTCCCGTGGAG 124
 Db 16632 TGTGGCCATCTTCTGGTCATCTGTGGTGGCGGCGACATGCGAGGCTCGGAGCCTCAGAG 16691
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RESULT 26
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 VERSION AC010965.12 GI:25103671
 KEYWORDS HTG; HTGS PHASE2; HTGS FULLTOP; HTGS_ACTIVEFIN.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 AUTHORS
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
 Baldwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Boukhgalter, B.,
 Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
 Cooke, P., DeArelano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
 Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D.,
 Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
 Howland, J., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
 Lehoczy, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,
 McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,
 Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
 Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
 Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
 Teefaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
 Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (28-SEP-1999) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 186208)

REFERENCE
 AUTHORS
 Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B.,
 Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
 Cook, A., Cooke, P., DeArelano, K., Dewar, K., Diaz, J.S., Dodge, S.,
 Faros, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,
 Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N.,
 Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
 Kanat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
 Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J.,
 Matthews, C., McCarthy, M., Meldrim, J., Meneus, D., Mihova, T.,
 Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
 Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,

TITLE
 JOURNAL

COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WITBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 Project Information
 Center project name: L908
 Center Clone name: 479 L_21

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 2 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 176982: contig of 176982 bp in length
 * 176983 177082: gap of 100 bp
 * 177083 186208: contig of 9126 bp in length.

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Query Match 8.4%; Score 228.4; DB 2; Length 186208;
 Best Local Similarity 81.3%; Pred No. 7.9e-33;
 Matches 265; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Qy 5 TCCTGGGCGCAGCTGTCGCCGCCAGCATCGCGGAGCAGCCTTCTATGTATACAGCAGC 64
 Db 125723 TTGTTGGAGCAGCCTCCCAAGCCCGAGTGCCTGAGGCGCTTCCATGTACGCGACTGC 125782

Qy 65 AGTGGCCATCTTCTGGTCATCTGTGGTGGCGGACATGCGAGGCTCGGCTCCCGTGGAG 124
 Db 125783 TGTGGCCATCTTCTGGTCATCTGTGGTGGCGGACATGCGAGGCTCGGAGCTCCAGAGAG 125842

Qy 125 CCCCCTCCCTATCACATCCCCCTGGACCCCGAGGGTCCCTGGAGCTCTCATGGAATGT 184
 Db 125843 CCCCCTCCCTATCACATCCCCCTGGACCCCGAGGGATTTAGAGCTCTCATGGAACGT 125902

Qy 185 CAGCTACACCCAGGAGGCCATCCATTTCCAGCTCCTGGTGGGAGGCTCAAGGCTGGCGT 244
 Db 125903 CAGCTATGCCAGGAGATCATCTTCCAGCTCCAGGTCAGGCTGAGGCTGGGCT 125962

Qy 245 CTTCTTTGGAGTCCGACCGTGGCGAGCTTGAGAGCGAGATCTCTGGTGTCTCTGGAC 304
 Db 125963 CTTCTTTGGAGTCCGACCGTGGCGAGCTTGAGAGCGAGATCTCTATCATGTCTCTGGAC 126022

Qy 305 CGATGGGACACTGCCTATTTTGGG 330
 Db 126023 TGATGGGACAGGCGCTACTTTTGGG 126048

RESULT 27
AC091762/c
LOCUS
DEFINITION
AC091762 205420 bp DNA linear HTG 11-JUN-2003
Mus musculus clone rp23-151n4 map 2 strain C57BL/6J, WORKING DRAFT
SEQUENCE, 2 ordered pieces.
AC091762
AC091762.26 GI:31581643
HTG; HTGS PHASE2; HTGS DRAFT.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Jiang, X., Song, L. and Roe, B.A.
Mus musculus Chromosome 10 BAC Clone rp23-151n4
Unpublished
2 (bases 1 to 205420)
Jiang, X., Song, L. and Roe, B.A.
Direct Submission
Submitted (31-MAY-2001) Department of Chemistry And Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
3 (bases 1 to 205420)
Jiang, X., Song, L. and Roe, B.A.
Direct Submission
Submitted (11-JUN-2003) Department of Chemistry And Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
On Jun 11, 2003 this sequence version replaced gi:31560185.
----- Genome Center
Center: Department of Chemistry And Biochemistry
The University of Oklahoma
Center code:UOKNOR

* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 1 21604: contig of 21604 bp in length
* 21605 21704: gap of unknown length
* 21705 205420: contig of 183716 bp in length.
Location/Qualifiers
1..205420

FEATURES

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/map="2"
/clones="rp23-151n4"
/clone_lib="RPCI - 23 Female (C57BL/6J) Mouse BAC Library"

BASE COUNT 51372 a 53298 c 51045 g 49605 t 100 others
ORIGIN

Query Match 8.4%; Score 228.4; DB 2; Length 205420;
Best Local Similarity 81.3%; Pred. No. 7.8e-33;
Matches 265; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 5 TCGTGGCCGAGCTGCCGCGCCAGCATGCGGAGGAGCGCTTCATGTACAGCACGC 64
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QY 65 AGTGGCCATCTTCGTGTATCTGTGGCCGACATGCGAGGGCTCGGCTCCCGGTGAGAG 124
Db 59359 TGTGGCCATCTTCGTGTATCTGTGGCTGCTGCTGCGGGCTCGGAGCTCCAGAG 59300
QY 125 CCCCTCCCTATCATCCCCCTGACCGGAGGGTCCCTGGAGCTCTCATGGAATGT 184
Db 59299 CCCTTCCCTACCATCCCCCTGACCCCGAAGGATTTTAGAGCTCTCATGGAAGCT 59240

QY 185 CAGTACACCCAGGAGGCCATCCATTTCCAGCTCCCTGGTCCGGAGGCTCAAGCGTGGCGT 244
Db 59239 CAGCTATGTCCAGAGAGATCATCCATTTCCAGCTCCAGGTCGAAGGCTGAGGGCTGGGGT 59180
QY 245 CTTGTTGGGATGTCGACCCGTGGCGGAGTGTGAGAACGCGAGATCTCGTGTGCTCTGGAC 304
Db 59179 CTTGTTGGGATGTCAGATCGAGGAGATGGAGAACGCGAGATCTCATCATGCTCTGGAC 59120
QY 305 CGATGGGACACTGCCTATTTCGGG 330
Db 59119 TGATGGGACAGGCGCTACTTTCGGG 59094

RESULT 28

AF075385

LOCUS

DEFINITION

AF075385 663 bp mRNA linear VRT 17-JUN-1999

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Danio rerio (zebrafish)

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 663)

Guo, S., Wilson, S.W., Cooke, S., Chitnis, A.B., Driever, W. and

Rosenthal, A.

Mutations in the zebrafish unmask shared regulatory pathways

controlling the development of catecholaminergic neurons

Dev. Biol. 208 (2), 473-487 (1999)

99208650

2 (bases 1 to 663)

Guo, S. and Rosenthal, A.

Direct Submission

Submitted (29-JUN-1998) Neuroscience, Genentech Inc., 1 DNA Way,

South San Francisco, CA 94080, USA

Location/Qualifiers

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/organism="Danio rerio"

/mol_type="mRNA"

/db_xref="taxon:7955"

<1..>663

/gene="dbh"

<1..>663

/gene="dbh"

/codon_start=1

/product="dopamine beta hydroxylase precursor"

/protein_id="AAD34219.1"

/db_xref="GI:4959065"

/translation="GPCRDMKPRNLNRYHVLAAWAGAEFFYPADAGLPMGGES

SRFLRLVHNPLLSGRDSSGIRLWYSPRRFDAGIMELGLVTVPMVAPRRQR

SFQLTGYCTAKCTOTALPSRGHTLCLPAHSSRSWGQCLGARRSRXXGARRTDI

SSHYQIIRVLHWVTGLPYRCSAHXVADSNTRGTXYKXVCGXGFGNMGCMCRQXNV

PKA"

BASE COUNT 144 a 165 c 180 g 165 t 9 others

ORIGIN

Query Match 8.1%; Score 221.6; DB 5; Length 663;

Best Local Similarity 66.6%; Pred. No. 3.7e-31;

Matches 359; Conservative 0; Mismatches 177; Indels 3; Gaps 3;

QY 831 GGGCCCTGCCACTCCAGATGAACCGACCGCTCACTACGCCGCCACGTGGCC 890

Db 1 GGGCCGTGTGATGGAAGATGAAGCGCGCAATCTTAATTAATTCAGACATGTTCTGGCT 60

QY 891 GCCTGGCCCTGGGTGCCAAGGCAATTTACTACCCAGAGGAAGCCGCGCTTGCCTTCGGG 950

Db 61 GCCTGGCCCATGGGAGCAGACCATCTACTACTCTGCTGACGCTGTTTGCCTATGGGA 120

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Qy 951 GGTCCAGGGTCTCCAGATATCTCGCTCGGAGTTCATACCAACCCCACTCGGTGATA 1010
Db 121 GGAGAGGATCTTCTAGGTTTCTTCGTCTTGAAGTTTCAATACCAACCCCTCTCTTTTA 180
Qy 1011 GAAGGACGAACGACTCTCTCAGGATCGCTTGTACTACACAGCAAGCTCGGGGCTTC 1070
Db 181 TCAGGGCGGAGGACTCTCTCGGATTCGTTTATGTGTACATCCTCTCTCGGAGGTTT 240
Qy 1071 AACCGGGGATCATGGAGCTGGGACTGGTGTATACAGCGCAGTGATGGCCATTCACCCACGG 1130
Db 241 GACGAGGATCATGGAGCTGGGCTGGTGTATACACTCTCTGTATGGCCATTCCTCCCCCGC 300
Qy 1131 GAGACCGCTTCATCTCAGTCTGCTGACGACGACGAAGTGCACCGAGCTGGCACTGCCT 1190
Db 301 CAGCGCTCTTTCACGACTCAGTGGATCTGCAACCGCAAAATGCACAGACAGCGCTCTTCCA 360
Qy 1191 CCCTCCGG-ATCCACATCTTCGCTCTCAGCTCCACACACTGACTGGGAAAGGT 1249
Db 361 AGTAGGGGACATACATCTTTCGCTCCAGCTGCACACTCATCTGGCGGTCTTGGGGT 420
Qy 1250 GGTCCAGTGTCTCGGAGCGCGCGGAGTGGAGATCTGTG-AACGAGACATCACT 1308
Db 421 CAGGACTGTCTTGGTGGAGGAGTCAAGANGTGNAGTGTGCAAGGAGACAGACATT 480
Qy 1309 AC-AGCCCTCACTCCAGGAGATCGGATGTTGAAGAGTGTGTCGTCATCCCGG 1366
Db 481 TCAAGCACATTAACCAAGATCATCCGTGTTTATACATGAAGTGTGACTGGTCTGCCANG 539

RESULT 29
AC126203
LOCUS
DEFINITION Rattus norvegicus clone CH230-177E3, WORKING DRAFT SEQUENCE, 2
unordered pieces.
AC126203
AC126203.3 GI:25007867
HTG; HTGS, PHASE1; HTGS DRAFT; HTGS_FUL1TOP.
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 225079)
Muzny,D,Marle., Metzker,M, Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alebrooks,S., Amin,A., Anquiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Cesar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Evans,C.A., Falls,T., Fan,G.,
Egan,A., Escotto,M., Eugene,C., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Harvey,J., Havlak,P., Haves,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowitz,C., Kraft,C., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorenshewa,L., Louleghed,H., Lozada,R.J., Lu,X., Ma,J.,
Maheehwari,M., Mahindartine,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
```

Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwokenleh,O., Okwuonu,G., Olarinpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L., L., Puzo,M., Quirroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojao,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shateman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Soosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villaseana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhauser,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

Unpublished
2 (bases 1 to 225079)
Worley,K.C.
Direct Submission
Submitted (04-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 225079)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 15, 2002 this sequence version replaced gi:22196254.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GZGS
Center clone name: CH230-177E3
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 191488 bases at least Q40
Consensus quality: 194511 bases at least Q30
Estimated insert size: 199941; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 223772: contig of 223772 bp in length

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* 223773 223872: gap of unknown length
* 223873 225079: contig of 1207 bp in length.
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            /clone="CH230-177E3"
            /note="wgs contig"
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        46863 a 51393 c 52190 g 47818 t 26815 others
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        Query Match
        Best Local Similarity 81.0%; Score 220; DB 2; Length 225079;
        Matches 256; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
    QY
        15 AGCTGCCCCGCCAGCATGGGAGGAGCAGCTTCATGTACAGACAGCAGTGGCCATC 74
        Db
        165644 AGCTCCCCAGCCCCAGCGTCGCGTGGGCGGCTTCATGTATGGCACTGCTGTGGCCATC 165703
    QY
        75 TTCCTGGTTCATCTGCTGGCCGCACTGCAGGGCTCGGCTCCCGTGAGAGCCCTCCGAGAGCCCTTCCCT 165763
        Db
        165704 TTCCTGGTTCATCTGCTGGTGCATCTGAGGCTCGAGGCTCGAGAGCCCTCCGAGAGCCCTTCCCT 165763
    QY
        135 TATACATCCCCCTGGACCCGAGGGGTCCCTGGAGCTCTCATGGAATGTTCAGCTACACC 194
        Db
        165764 TACCACATCCCCCTGGACCCCTGAAGGACTTTAGAGCTCTCGTGAACGTTCAGCTATGAC 165823
    QY
        195 CAGGAGGCCATCATTTCCAGCTCTGCTGGGAGGCTCAAGGCTGGCGTCTCTTTGGG 254
        Db
        165824 CAGGAGATCATCCACTTCAGCTCCAGTCCAGGTCAAGGGCGGAGGGTGGGCTCTTCCGA 165883
    QY
        255 ATGTCCGACCGTGGAGCTTTGAGAACGACAGATCTCGTGGTGTCTCGACCGATGGGGAC 314
        Db
        165884 ATGTCCGATCAGGTGAGATGAGATGAGAACGACACCTCGTCTGATCTGATCTGACGGGGAC 165943
    QY
        315 ACTGCTATTTTGGG 330
        Db
        165944 AGGACCTACTTTGGG 165959
    RESULT 30
    AX347199/c
    LOCUS
    DEFINITION
    Sequence 2270 from Patent WO0200928.
    ACCESSION
    AX347199
    VERSION
    AX347199.1 GI:18495087
    KEYWORDS
    .
    SOURCE
    synthetic construct
    synthetic construct
    artificial sequences.
    ORGANISM
    .
    REFERENCE
    1
    Olek,A.; Piepenbrock,C. and Berlin,K.
    Diagnosis of diseases associated with the immune system
    JOURNAL
    Patent: WO 0200928-A 2270 03-JAN-2002;
    Epigenomics AG (DE)
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    Location/Qualifiers
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    1..2037
    /organism="synthetic construct"
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    /db_xref="taxon:32630"
    /note="chemically treated genomic DNA (Homo sapiens)"
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    Query Match
    Best Local Similarity 7.1%; Score 193; DB 6; Length 2037;
    Matches 244; Conservative 0; Mismatches 85; Indels 0; Gaps 0;
    QY
    1 TCAGTCGCTGGGCGACGCTGCGCGGCCCGCCAGCATGGGGAGGAGGCTTCATGTACAGCA 60
    Db
    338 TCAATCGCTAAACCAACCTACCCGACCCCAACATACGAAAAACAACCTTCATATACAACA 279
    QY
    61 CAGCAGTGGCCATCTTCCTGGTTCATCTGCTGGTGGCCGACATGCGAGGCTGGCTCCCGGTG 120
    Db
    278 CAACAATAACCAATCTTCCTTAATCATCTAATAACCGCACTACAAAACTGACTTCCCGCGTA 219
    QY
    121 AGAGCCCTCCCTTCATCATATCCCTGGACCCGAGGGGTCCCTGGAGCTCTCATGGA 180
    Db
    218 AAAACCCCTCCCTTCATCATATCCCTTAACCCGAAAAATCCCTTAAACTCTCATATA 159
    QY
    181 ATGTCACTACACCCAGGAGGCTCCATTTCCAGCTCTGCTGGTGGAGGCTCAAGGCTG 240
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    158 ATATCACTACACCCAAAAAACCATTCATTTCACTTCACTTAATACGAAAACTCAAAACTA 99
    QY
    241 GCCTCTGTTTGGATGTCCGACCGGTGGAGCTTGAGAACGACATCTCGTGGTCTCT 300
    Db
    98 ACCTCTATTATTAATATATCCGACCGGTAAACGAACTTAAAAACGCAATCTCGTAATACTCT 39
    QY
    301 GGACCATGGGACACTGCCTATTTTGGG 329
    Db
    301 GGACCATGGGACACTGCCTATTTTGGG 329
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    LOCUS
    DEFINITION
    Sequence 40 from Patent WO0202809.
    ACCESSION
    AX348532
    VERSION
    AX348532.1 GI:18614567
    KEYWORDS
    .
    SOURCE
    synthetic construct
    synthetic construct
    artificial sequences.
    ORGANISM
    .
    REFERENCE
    1
    Olek,A.; Piepenbrock,C. and Berlin,K.
    Diagnosis of behavioural disorders, neurological disorders and
    cancer
    JOURNAL
    Patent: WO 0202809-A 40 10-JAN-2002;
    Epigenomics AG (DE)
    FEATURES
    Location/Qualifiers
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    1..2037
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"
    /note="chemically treated genomic DNA (Homo sapiens)"
    BASE COUNT
    417 a 49 c 558 g 1013 t
    ORIGIN
    Query Match
    Best Local Similarity 7.1%; Score 193; DB 6; Length 2037;
    Matches 244; Conservative 0; Mismatches 85; Indels 0; Gaps 0;
    QY
    1 TCAGTCGCTGGGCGACGCTGCGCGGCCCGCCAGCATGGGGAGGAGGCTTCATGTACAGCA 60
    Db
    338 TCAATCGCTAAACCAACCTACCCGACCCCAACATACGAAAAACAACCTTCATATACAACA 279
    QY
    61 CAGCAGTGGCCATCTTCCTGGTTCATCTGCTGGTGGCCGACATGCGAGGCTGGCTCCCGGTG 120
    Db
    278 CAACAATAACCAATCTTCCTTAATCATCTAATAACCGCACTACAAAACTGACTTCCCGCGTA 219
    QY
    121 AGAGCCCTCCCTTCATCATATCCCTGGACCCGAGGGGTCCCTGGAGCTCTCATGGA 180
    Db
    218 AAAACCCCTCCCTTCATCATATCCCTTAACCCGAAAAATCCCTTAAACTCTCATATA 159
    QY
    181 ATGTCACTACACCCAGGAGGCTCCATTTCCAGCTCTGCTGGTGGAGGCTCAAGGCTG 240
    Db
    158 ATATCACTACACCCAAAAAACCATTCATTTCACTTCACTTAATACGAAAACTCAAAACTA 99
    QY
    241 GCCTCTGTTTGGATGTCCGACCGGTGGAGCTTGAGAACGACATCTCGTGGTCTCT 300
    Db
    98 ACCTCTATTATTAATATATCCGACCGGTAAACGAACTTAAAAACGCAATCTCGTAATACTCT 39
    QY
    301 GGACCATGGGACACTGCCTATTTTGGG 329
    Db
    301 GGACCATGGGACACTGCCTATTTTGGG 329
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Db      38 AAACCGATAAAACACTACCTATTATTACG 10

RESULT 32
HSDBH4
LOCUS   Human DNA for dopamine beta-hydroxylase exon 4 (EC 1.14.17.1).
DEFINITION
ACCESSION X13260.1 GI:30465
VERSION   alternative splicing; dopamine beta-hydroxylase; hydroxylase.
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 195)
AUTHORS  Kobayashi,K., Kurosawa,Y., Fujita,K. and Nagatsu,T.
TITLE    Human dopamine beta-hydroxylase gene: two mRNA types having
          different 3'-terminal regions are produced through alternative
          polyadenylation
JOURNAL  Nucleic Acids Res. 17 (3), 1089-1102 (1989)
MEDLINE  89160241
PUBMED   2922261
REFERENCE 2 (bases 1 to 195)
AUTHORS  Nagatsu,T.
TITLE    Direct Submission
JOURNAL  Submitted (14-OCT-1988) Nagatsu T., Department of Biochemistry,
          Nagoya University, School of Medicine, Nagoya 466, Japan
COMMENT  Map data from Craig et al. Cytogenet. Cell Genet. 48:48-50(1988).
FEATURES
source    1..195
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           /note="Exon 4"
           187..>195
           /note="Intron IV (ca 0.8 kb)"
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intron
mRNA
intron
BASE COUNT 37 a 75 c 52 g 31 t
ORIGIN

Query Match 6.6%; Score 180; DB 9; Length 195;
Best Local Similarity 100.0%; Pred. No. 2.6e-23;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 733 AGTACGAGCCCATCGTCACCAAGGGCAATGAGGCCCTTGTCACCAATGGAAGTCTTCC 792
Db 8 AGTACGAGCCCATCGTCACCAAGGGCAATGAGGCCCTTGTCACCAATGGAAGTCTTCC 67

Qy 793 AGTGCGCCCGGAGATGGACAGCGTCCCGACTTCAGCGGGCCCTGCGACTCCCAAGATGA 852
Db 68 AGTGCGCCCGGAGATGGACAGCGTCCCGACTTCAGCGGGCCCTGCGACTCCCAAGATGA 127

Qy 853 AACCCGACCGCCTCAACTACTGCGCCGACAGTGTGGCGCGCTGGCGCCCTGGGTGCCAAGG 912
Db 128 AACCCGACCGCCTCAACTACTGCGCCGACAGTGTGGCGCGCTGGCGCCCTGGGTGCCAAGG 187

RESULT 33
AX347198
LOCUS   Sequence 2269 from Patent WO0200928.
DEFINITION
ACCESSION AX347198
VERSION   AX347198.1 GI:18495086
KEYWORDS  synthetic construct
SOURCE    synthetic construct
ORGANISM  synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS  Olek,A., Piepenbrock,C. and Berlin,K.
TITLE    Diagnosis of diseases associated with the immune system
JOURNAL
FEATURES
source    1..2037
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           /mol_type="genomic DNA"
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           /note="chemically treated genomic DNA (Homo sapiens)"
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BASE COUNT 417 a 49 c 645 g 926 t
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Best Local Similarity 71.5%; Pred. No. 2.1e-23;
Matches 236; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

Qy 1 TCAGTCGCTGGGCCAGCCTGCCCGGCCCCAGCAGTCGCGGAGGAGCCCTTCATGTACAGCA 60
Db 1700 TTAGTCGTTGGGTAGTTTGTTCGGTTTATAGTATGCGGGAGGTAGTTTATATGATAGTA 1759

Qy 61 CAGCAGTGGCCATCTTCCTCGTTCATCTCGTGGCGGCACCTGCAGGGCTCGGCTCCCGGTG 120
Db 1760 TAGTAGTGGTTATTTTGTGTTATTTTGTGTTATTTGTAGGTTCGGTTTTCGTG 1819

Qy 121 AGAGCCCCCTCCCTATCATCATCCCTCGACCCGAGGGGTCCCTGGAGCTCTCATGGA 180
Db 1820 AGAGTTTTTTTTTTTATTATATATTTTGTGATTGCGAGGGGTTTTTGGAGTTTTTATGGA 1879

Qy 181 ATGTCAGTACACCCAGGAGCCATCCATTTCCAGCTCCTGTCGCGAGGCTCAAGCTG 240
Db 1880 ATGTTAGTTATATTTAGGAGGTATTTATTTTATTTTGGTGGGAGGTTTAAAGTTG 1939

Qy 241 GCGTCCTGTTTGGGATGTCGCGACCGTCGCGAGCTTGAGAACGACGAGATCTCGTGGTCT 300
Db 1940 GCGTTTGTGTTGGAGTTCGATCGTGGCGAGTTTGAGACCTAGATTTTCGTGTTT 1999

Qy 301 GGACCGATGGGACACCTGCCTATTTTGGCG 330
Db 2000 GGATCGATGGGATATTTGTTATTTTGGCG 2029

RESULT 34
AX348531
LOCUS   Sequence 39 from Patent WO0202809.
DEFINITION
ACCESSION AX348531
VERSION   AX348531.1 GI:18614566
KEYWORDS  synthetic construct
SOURCE    synthetic construct
ORGANISM  synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS  Olek,A., Piepenbrock,C. and Berlin,K.
TITLE    Diagnosis of behavioural disorders, neurological disorders and
          cancer
JOURNAL  Patent: WO 0202809-A 39 10-JAN-2002;
          Epigenomics AG (DE)
FEATURES
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           /mol_type="genomic DNA"
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           /note="chemically treated genomic DNA (Homo sapiens)"
           417 a 49 c 645 g 926 t

BASE COUNT 417 a 49 c 645 g 926 t
ORIGIN

Query Match 6.6%; Score 179.6; DB 6; Length 2037;
Best Local Similarity 71.5%; Pred. No. 2.1e-23;
Matches 236; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

Qy 1 TCAGTCGCTGGGCCAGCCTGCCCGGCCCCAGCAGTCGCGGAGGAGCCCTTCATGTACAGCA 60
Db 1700 TTAGTCGTTGGGTAGTTTGTTCGGTTTATAGTATGCGGGAGGTAGTTTATATGATAGTA 1759

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Qy 61 CAGCAGTGGCCATCTTCTCGTTCATCTGTCGCCGCACTGCGAGGCTCGCTCCCGCG 120
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1760 TAGTAGTGGTTATTTTGGTTATTTGGTTCGTAATTTAGGGTTCGGTTTTCGTCG 1819
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Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1820 AGAGTTTTCCTTATTTATTTTTCGATTCGGAGGGGTTTTCGAGTTCATGGA 1879
Qy 181 ATCTAGCTACACCCAGGAGGCCATTCATTCAGCTCTCTGTCGGAGGCTCAAGGCTG 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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2000 GGATCGATGGGATATTTTATTTTCGG 2029

RESULT 35
BC037684
LOCUS Mus musculus, RIKEN cDNA 3230402N08 gene, clone IMAGE:3675929,
DEFINITION mRNA
ACCESSION BC037684
VERSION BC037684.1 GI:23337062
KEYWORDS Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2164)
Direct Submission
Submitted (13-SEP-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maekeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 80 Row: d Column: 5
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 10946925.
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Best Local Similarity 46.8%; Pred. No. 1.1e-22;
Matches 703; Conservative 0; Mismatches 782; Indels 18; Gaps 4;
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27 TGTGCGCTGGCCACTGCTGTGCTGTGGTGTCTCCCGCGACGGCTGGGGGAGCC 86
Qy 127 CCCTCCCTCATCATCTCCCTCGACCCGAGGGGTCCTGGAGCTCTCATGGAATGTCA 186
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
87 CGGGCGCTCGTACCCGACCGGTGCTCTGATCCCGAAGCAAGTACTGGTGCAT 146
Qy 187 GCTACACCCAGGAGGCCATTCATTTCCAGCTCTCTGTCGGAGGCTCAAGGCTGGCTCC 246
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
147 GGGCGCGGAGGCTGAGAGGCTGGCTTCCTGCTGGAGTACGCACGACGGCTAGTGG 206
Qy 247 TGTTCGGATGTCGACCGTGGGAGCTTGAGAACGACGATCTCTGTGTGCTCTGGAACG 306
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
207 GCTTCGGCTTCGCGCCACCGGAGCATGGCGCGCAGACATCTGTGTGTAGCGGAGTGG 266
Qy 307 ATGGGACACTCGCTATTTTTCGGAGCGCTGGAGTGACAGAGGGGCGAGATCCACCTGG 366
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
267 CCCACGGCGGCTTACCTCCAGGACTATTTACAAAACGACAGACAGAGTTGGAAGAAG 326
Qy 367 ATCCCGCAGCAGACTACAGCTGCTGAGGTGACAGAGACCCAGAGGCTGACCTTCG 426
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
327 ATGCCAGCAGATATACCACTAGATTATGTCATGGAGAACAGACACACACAGTATCG 386
Qy 427 TTTTCAAGAGGCGCTTTGGCAGCTCGACCCCAAGGATTACCTCATTTGAAGACGCGATG 486
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
387 AGTTTAGCAGGAGCTGCACAGTGCATGCAATGACAGAGTCTACGGATAGCAGCG 446
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447 TGAGAGTTATCTGGGCTTACCACCATGACATCCCGAGATCTGTGTCCTCC---AAGTACC 503
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504 ATGACTTAATAGGGGACAGAGGCTGACGGTTACTGAAATCTCTGAGAAAGCCAA---TG 560
Qy 607 AGTTGCCCTCAGACCGCTGCACCATGGAGTCCAAAGCTCCCAATATCCAGATCCCGAGCC 666
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
561 TGGTGTCTACAGTCTTACTGTACTTTTGATCTGGTAAATCAAAAGCTTCCCATTCCAAACA 620
Qy 667 AGGAGACACGCTACTGTGCTACATTAAGAGCTTCCAAAGGGCTTCTCTCGGACCCACA 726
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
621 AAGCACAACATCTGTGTGCAATTTTAAAGATTCCTACATTCCAAGAAAAACATCATG 680
Qy 727 TTATCAAGTACAGCCCATCGTCAACAGGCAATGAGGCCCTTGTCCACCACCATGGAAG 786
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
681 TGATAAAGTGGAGCCAATAATAGAGAGGCCATGAAACCTGGTCCATCATCATCTGG 740
Qy 787 TCTTCCAGTGGCCCCCGAGATG---GACAGCTCCCCCACTTTCAGCGGCGCTCGGACT 843
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
741 TCTATCAATGACGAGCAACTTCAAGACAGCGTCTTGGACTTTGGCCATGAGTGTATC 800
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Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
801 ACCGACATGCCCGATGCTTCTCACCTGCGAAATCTGTGATTTCTGCGCTGGGGCATTTG 860
Qy 904 GTGCCAAGCATTTTACTATCCAGAGAGAACCGGCGCTTGCCTTTCGGGGGTTCAGGGGTCT 963
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
861 GTGAGAGGGCTTTTACTATCCACCTCACTGTTGGCTTATCCCTCGGATGCCACTGGATC 920
Qy 964 CCAGATATCTCCGCTGGAGGTTCTACCAACCACTGGTGATAGAGGACGAAACG 1023

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arose spontaneously from a senescent normal mammary
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/notes="Vector: pCMV-SPORT6"

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Db      981 ACAGTTCGGGCTGAGGGTTTCCNATACTACAGATATAAGAGATATACGCGAGAGTGA 1040
Qy      1084 TGGAGCTGGGACTGGGTATACAGCGCAGTATGCGCATTCACACCGGAGACCGCTTCA 1143
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Qy      1144 TCCTCACTGGCTACTGACGAGCAAGTGCACCCAGCTGGCACT-----GCTCCT 1194
Db      1101 ATTCTGAGGGTCACTGCACTCTGAGTGCCTAGAGGAGCGCTGGGAGCTGAGAAACAA 1160
Qy      1195 CCGGGATCCACATCTTGGCTCTCAGCTCCAGTCCACACACCTGACTGGGAGAAAGTGTCA 1254
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Qy      1255 CAGTGTGGTCCGGGACGGCGGAGTGGGAGATCGTGAACCAAGACAATCACTACAGCC 1314
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Qy      1315 CTCATTCACGAGATCCGATGTTGAAGAGTGTGTCGGTCCATCCGAGAGATGTC 1374
Db      1281 TTAATTTCCAGGAGTTTCAGTATCTGAGGGAGAAACAAACAATCTTACCAGGTGATAACC 1340
Qy      1375 TCATCACCTCTGTCACGTACAAACGGAAGACCGGAGCTGGCCACAGTGGGGGCTTCG 1434
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Qy      1495 TCTGCAAGAGCGTGTGACGCGCGCTCTCTGCAAGATGACTTCCACTCATCAACAGGT 1554
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RESULT 36
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LOCUS   AB041606
DEFINITION Mus musculus brain cDNA, clone MNCB-5203.
ACCESSION AB041606
VERSION  AB041606.1 GI:7670475
KEYWORDS full (full insert sequence).
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Osada,N., Kusuda,J., Tanuma,R., Ito,A., Hirata,M., Sugano,S. and Hashimoto,K.
TITLE   isolation of full-length cDNA clones from mouse brain cDNA library made by oligo-capping method
JOURNAL Unpublished
AUTHORS Hashimoto,K., Osada,N., Kusuda,J. and Sugano,S.
TITLE   Direct Submission
JOURNAL Submitted (12-APR-2000) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
COMMENT (E-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)
URL: http://www.nih.go.jp/yoken/genebank/
Lib Name: Sugano mouse brain mncb
Lab host: TOP10
Vector:   pME18S-FL3

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1st strand cDNA was primed with an oligo(dT) primer [ATGCGCCTTTTTTTTTTTTTT]; double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with SfiI and size selection was performed to exclude fragments <1.5kb. The SfiI-digested PCR product was cloned into distinct DraIII sites of pME18S-FL3. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Library was constructed by Sugano et al. (University of Tokyo, Institute of Medical Science). Custom primer used for sequencing (5' end primer [CTTCTGCTCTAAAGCTGCG]; 3' end primer [CGACTGCGCTCAGACACA]).

A part of this sequence is reported in AU080082.

FEATURES

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AVMTWGLSTRNEMCLSYLLYPRVNLTRCSSPIDMEQLQFIVGKXIYRPTVTPPI
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BASE COUNT 748 a 710 c 710 g 735 t
ORIGIN

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Query Match      6.4%; Score 174.2; DB 10; Length 2903;
Best Local Similarity 46.7%; Pred. No. 2e-22;
Matches 702; Conservative 0; Mismatches 783; Indels 18; Gaps 4;

Qy      67 TGGCCATCTTCCTGGTCACTCTGTCGCGCCCATCGAGGCTCGGCTCCCGTGAGAGCC 126
Db      24 TGTGCGGCTGGCCACTGCTTGCTGTGGCGCTGCTCCCGCGAGCGGTCGCGGAAGCC 83
Qy      127 CCCTCCCTATCATCATCCCCCTCGACCCGAGGGGTCCTCGAGCTCTCATGGAATGCA 186
Db      84 CGGGCGCTCGTACCCGACCGCGTGTCTCATCCGAGGCAAGTACTGGTGCCT 143
Qy      187 GTTACACCCAGGAGCCATCAATTTCCAGCTCTCTGGTGGAGAGCTCAAGGCTGGGCTCC 246
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Qy      247 TGTTCGGATGTCGACCGCTGGCGAGCTTGAGAACCCAGATCTCTGGTGTCTCTGACCCG 306
Db      204 GCTTCGGCTTCTCGCCACCGGAGCATGGCCCGCGCAGACATCGTGTGTGGGAGTGG 263
Qy      307 ATGGGACACTGCTTATTTTGGCGAGCGCTTGGAGTGACCAAGAGGGGCGAGATCCACCTGG 366
Db      264 CCCACGGGCGGCTTACTCCAGGACTATTTCAAAACGACAGAGAGTTGGAAAAAG 323
Qy      367 ATCCCGCAGGAGTACTACAGTGTCTCCAGTGCAGAGGACCCCGAGAGGCTGACCCCTGC 426
Db      324 ATGCCCAGCAAGATTACCACTAGATTACGCCATGAGAACACACACACAGTATCG 383
Qy      427 TTTTCAAGAGGCTTTGGCACCCTCGACCCCGCCAGGATTACCTCATTTGAAGAGCGCATG 486
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QY 487 TCCACTTGGTCTAGGAGTCTCGAGGAGCGGTTCCGGTCACTGGAGGCCATCAAGGCT 546
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QY 547 CGGGCTGCAGATGGGGTGCAGAGGTCAGCTCCTGAAGGCCAATATPCCCGAACCGG 606
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Db 1518 ACA 1520

RESULT 37

BC025892

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

FEATURES

source

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/tissue_type="Mammary tumor metastasized to lung. Tumor

BC025892 2796 bp mRNA linear ROD 16-APR-2003
Mus musculus RIKEN cdna 3230402N08 gene, mRNA (cdna clone
IMAGE:5038657), partial cds.

BC025892.1 GI:19483984

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 2796)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Udén, T.B., Toshiyuki, S.,
Carninci, P., Frange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahy, J., Helton, E., Kettman, M., Madan, A., Young, A.C., Rodrigues, S.,
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Rodrigues, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smalls, D.E.,
Schnerich, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

23388257

12477932

2 (bases 1 to 2796)

Strausberg, R.

Direct Submission

Submitted (13-MAR-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)

DNA Sequencing by: Baylor College of Medicine Human Genome

Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>Contact: amg@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseghe, H.,

Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,

A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>

Series: IRAC Plate: 45 Row: j Column: 21.

Location/Qualifiers


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JOURNAL Submitted (14-OCT-1988) Nagatsu T., Department of Biochemistry, Nagoya University, School of Medicine, Nagoya 466, Japan
COMMENT Map data from Craig et al. Cytogenet. Cell Genet. 48:48-50 (1988).
FEATURES Location/Qualifiers
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Db 8 AGGACGAACCACTCTCAGGATCCGCTTGCTACTACACGCCAAGCTGGCGCTTCAA 67

QY 1073 CGCGGGGATCATGGAGCTGGGACTGGTGTACACGCCAGTGATGCCATTCACACCGGA 1132
Db 68 CGCGGGGATCATGGAGCTGGGACTGGTGTACACGCCAGTGATGCCATTCACACCGGA 127

QY 1133 GACGCGCTTATCTCTACTGCTCTGTCACGCGAAGTGACCCAGCTGG 1182
Db 128 GACGCGCTTATCTCTACTGCTCTGTCACGCGAAGTGACCCAGCTGG 177

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VERSION AF129263.1 GI:4928110
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2906)
AUTHORS Gilbert,J.R., Kumar,A., Newey,S., Rao,N., Ioannou,P., Qiu,H., Lin,D., Xu,P., Pattenati,M.J. and Pericak-Vance,M.A.
TITLE Physical and cDNA mapping in the DBH region of human chromosome 9q34
JOURNAL Hum. Hered. 50 (3), 151-157 (2000)
MEDLINE 20153491
PUBMED 10686491
REFERENCE 2 (bases 1 to 2906)
AUTHORS Gilbert,J.R., Kumar,A., Newey,S. and Pericak-Vance,M.A.
TITLE Direct Submission
JOURNAL Submitted (18-FEB-1999) Center for Human Genetics, Duke University Medical Center, Research Park 2, DUMC, Durham, NC 27710, USA
FEATURES Location/Qualifiers
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Db 463 GTCAGCTGTCTCCCGCAGCTGGCTGTTCTTGTCCCGCCAGGTTCAACACGAGGATGTC 404

QY 1572 TGCACCTTGGCCCTCAGGCGTCCGTCTCAGCAGTTACCTCTGTTCCTTGGAACTCCTTC 1631
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QY 1632 AACCGCAGCTACTGAAGGCCCTGTACAGCTTCGCGCCCATCTCCATGCACTGCAACAAG 1691
Db 343 AACCGCAGCTACTGAAGGCCCTGTACAGCTTCGCGCCCATCTCCATGCACTGCAACAAG 284

QY 1692 TCCTCAGCGCTCGCTTCCAGG 1713
Db 283 TCCTCAGCGCTCGCTTCCAGG 262

RESULT 40
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LOCUS HSDBH11 178 bp DNA linear PRI 04-MAY-1990
DEFINITION Human DNA for dopamine beta-hydroxylase exon 11 (EC 1.14.17.1).
ACCESSION X13267
VERSION X13267.1 GI:30461
KEYWORDS alternative splicing; dopamine beta-hydroxylase; hydroxylase.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 178)
AUTHORS Kobayashi,K., Kurosawa,Y., Fujita,K. and Nagatsu,T.
TITLE Human dopamine beta-hydroxylase gene: two mRNA types having different 3'-terminal regions are produced through alternative polyadenylation
JOURNAL Nucleic Acids Res. 17 (3), 1089-1102 (1989)
MEDLINE 89160241
PUBMED 2922261
REFERENCE 2 (bases 1 to 178)
AUTHORS Nagatsu,T.
TITLE Direct Submission
JOURNAL Submitted (14-OCT-1988) Nagatsu T., Department of Biochemistry, Nagoya University, School of Medicine, Nagoya 466, Japan
COMMENT Map data from Craig et al. Cytogenet. Cell Genet. 48:48-50 (1988).
FEATURES Location/Qualifiers
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QY 1607 CACCTCTGTTCCCTGGAACTCCCTTCAACCGCGAGCTGTAAGGCCCTGTACAGCTTCGC 1666
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Qy 1667 GCCCATCTCCATGCACTGCAACAAGTCTCTCAGCCGTCGGCTTCCAGG 1713
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